SEQUENCE LISTING

<110> Chang, Chawnshang

<120> Androgen Receptor Coactivators
<130> 920920.90011

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<150> US 60/100,243
<151> 1998-09-14

<160> 47

<170> PatentIn Ver. 2.0

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      form a cystein-rich RING finger motif.

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<223> Coding sequence and polypeptide region for a
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ggtctctggt ctcccctctc tgagcactct gaggtcctt atg tcg tca gaa gat     54
                                               Met Ser Ser Glu Asp
                                               1               5


cga gaa gct cag gag gat gaa ttg ctg gcc ctg gca agt att tac gat    102
Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu Ala Ser Ile Tyr Asp
                10                  15                  20

gga gat gaa ttt aga aaa gca gag tct gtc caa ggt gga gaa acc agg    150
Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln Gly Gly Glu Thr Arg
            25                  30                  35

atc tat ttg gat ttg cca cag aat ttc aag ata ttt gtg agc ggc aat    198
Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile Phe Val Ser Gly Asn
            40                  45                  50

tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt    246
Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe
        55                  60                  65

ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc    294
Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser
70                  75                  80                  85

tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act    342
Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr
                90                  95                  100

cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac    390
Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His
                105                 110                 115

cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag    438
Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu
                120                 125                 130

acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt    486
Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly
        135                 140                 145

tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca    534
Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr
150                 155                 160                 165

gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa    582
Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu
                170                 175                 180
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2

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att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg    630
Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu
            185                 190                 195

atc cag gaa atc ttg gac ttt gat caa gct cag cag ata aaa tgc ttt    678
Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln Gln Ile Lys Cys Phe
            200                 205                 210

aat agt aaa ttg ttc ctg tgc agt atc tgt ttc tgt gag aag ctg ggt    726
Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe Cys Glu Lys Leu Gly
            215                 220                 225

agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc    774
Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala
230                 235                 240                 245

tgt ctg aag gac tac ttt gaa atc cag atc aga gat ggc cag gtt caa    822
Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg Asp Gly Gln Val Gln
            250                 255                 260

tgc ctc aac tgc cca gaa cca aag tgc cct tcg gtg gcc act cct ggt    870
Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser Val Ala Thr Pro Gly
            265                 270                 275

cag gtc aaa gag tta gtg gaa gca gag tta ttt gcc cgt tat gac cgc    918
Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe Ala Arg Tyr Asp Arg
            280                 285                 290

ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc    966
Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala Asp Val Val Tyr Cys
            295                 300                 305

ccc cgg ccg tgc tgc cag ctg cct gtg atg cag gaa cct ggc tgc acc    1014
Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln Glu Pro Gly Cys Thr
310                 315                 320                 325

atg ggt atc tgc tcc agc tgc aat ttt gcc ttc tgt act ttg tgc agg    1062
Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe Cys Thr Leu Cys Arg
            330                 335                 340

ttg acc tac cat ggg gtc tcc cca tgt aag gtg act gca gag aaa tta    1110
Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val Thr Ala Glu Lys Leu
            345                 350                 355

atg gac tta cga aat gaa tac ctg caa gcg gat gag gct aat aaa aga    1158
Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp Glu Ala Asn Lys Arg
            360                 365                 370

ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa    1206
Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile Gln Lys Ala Leu Glu
            375                 380                 385
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3

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gag atg gaa agt aag gag tgg cta gag aag aac tca aag agc tgc cca     1254
Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn Ser Lys Ser Cys Pro
390             395             400             405

tgt tgt gga act ccc ata gag aaa tta gac gga tgt aac aag atg aca     1302
Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly Cys Asn Lys Met Thr
                410             415             420

tgt act ggc tgt atg caa tat ttc tgt tgg att tgc atg ggt tct ctc     1350
Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile Cys Met Gly Ser Leu
            425             430             435

tct aga gca aac cct tac aaa cat ttc aat gac cct ggt tca cca tgt     1398
Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp Pro Gly Ser Pro Cys
            440             445             450

ttt aac cgg ctg ttt tat gct gtg gat gtt gac gac gat att tgg gaa     1446
Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp Asp Asp Ile Trp Glu
            455             460             465

gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg           1494
Asp Glu Val Glu Asp
470             475

ctcaagatat ggaagtggat tgttttccc taatcttccg tcaagtacac aaagtaactt  1554

tgcgggatat ttagggtact attcattcac tcttcctgcg tagaagatat ggaagaacga  1614

ggtttatatt ttcatgtggt actactgaag aaggtgcatt gatacatttt taaatgtaag  1674

ttgagaaaaa tttataagcc aaaggttcag aaaattaaac tacagaa               1721
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<213> Homo sapien

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 1               5              10              15

Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln
            20              25              30

Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile
        35              40              45

Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu
    50              55              60
```

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Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro
65              70              75                      80

Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys
                85                  90                  95

Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn
            100             105             110

Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln
        115             120                 125

Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe
130             135             140

Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln
145             150             155                 160

Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp
                165             170             175

Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu
            180             185             190

Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln
        195             200             205

Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe
210             215             220

Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His
225             230             235             240

Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg
            245             250             255

Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser
            260             265             270

Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe
            275             280             285

Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala
        290             295             300

Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln
305             310             315             320

Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe
                325             330             335
```

                                    5

Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val
              340   345   350

Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp
          355   360   365

Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile
    370   375   380

Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn
385   390   395   400

Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly
              405   410··   415
Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile
              420   425   430   .

Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp
          435   440   445

Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
    450   455   .460   .

Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
465   470

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Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
  1               5                  10                  15


cct ccc cca tcc tat ggc cac cag cca aca ggg cag tct ggg gag tct    96
Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
                 20                  25                  30


tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag   144
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
             35                  40                  45


cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct   192
Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser
         50                  55                  60


tcc agc ggt gtc ttg ggt acc ggg ctc tgt gag cta gat cgg ttg ctt   240
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu
 65                  70                  75                  80


cag gaa ctt aat gcc act cag ttc aac atc aca gat gaa atc atg tct   288
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser
                 85                  90                  95


cag ttc cca tct agc aag gtg gct tca gga gag cag aag gag gac cag   336
Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln
                100                 105                 110


tct gaa gat aag aaa aga ccc agc ctc cct tcc agc ccg tct cct ggc   384
Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly
            115                 120                 125
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ctc cca aag gct tct gcc acc tca gcc act ctg gag ctg gat aga ctg    432
Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu
    130             135             140

atg gcc tca ctc cct gac ttc cgc gtt caa aac cat ctt cca gcc tct    480
Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser
145             150             155             160

ggg cca act cag cca ccg gtg gtg agc tcc aca aat gag ggc tcc cca    528
Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro
            165             170             175

tcc cca cca gag ccg act gca aag ggc agc cta gac acc atg ctg ggg    576
Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly
        180             185         ··      190

ctg ctg cag tcc gac ctc agc cgc cgg ggt gtt ccc acc cag gcc aaa    624
Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys
        195             200             205

ggc ctc tgt ggc tcc tgc aat aaa cct att gct ggg caa gtg gtg acg    672
Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr
    210             215             220

gct ctg ggc cgc gcc tgg cac ccc gag cac ttc gtt tgc gga ggc tgt    720
Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys
225             230             235         .           240

tcc acc gcc ctg gga ggc agc agc ttc ttc gag aag gat gga gcc ccc    768
Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro
            245             250             255

ttc tgc ccc gag tgc tac ttt gag cgc ttc tcg cca aga tgt ggc ttc    816
Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe
        260             265             270

tgc aac cag ccc atc cga cac aag atg gtg acc gcc ttg ggc act cac    864
Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His
        275             280             285

tgg cac cca gag cat ttc tgc tgc gtc agt tgc ggg gag ccc ttc gga    912
Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly
    290             295             300

gat gag ggt ttc cac gag cgc gag ggc cgc ccc tac tgc cgc cgg gac    960
Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp
305             310             315             320

ttc ctg cag ctg ttc gcc ccg cgc tgc cag ggc tgc cag ggc ccc atc   1008
Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile
        325             330             335
```

8

```
ctg gat aac tac atc tcg gcg ctc agc ctg ctc tgg cac ccg gac tgt     1056
Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys
            340             345             350

ttc gtc tgc agg gaa tgc ttc gcg ccc ttc tcg gga ggc agc ttt ttc     1104
Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe
            355             360             365

gag cac gag ggc cgc ccg ttg tgc gag aac cac ttc cac gca cga cgc     1152
Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg
        370             375             380

ggc tcg ctg tgc ccc acg tgt ggc ctc cct gtg acc ggc cgc tgc gtg     1200
Gly Ser Leu Cys Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val
385             390             395             400

tcg gcc ctg ggt cgc cgc ttc cac ccg gac cac ttc gca tgc acc ttc     1248
Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe
            405             410             415

tgc ctg cgc ccg ctc acc aag ggg tcc ttc cag gag cgc gcc ggc aag     1296
Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys
            420             425             430

ccc tac tgc cag ccc tgc ttc ctg aag ctc ttc ggc tga                 1335
Pro Tyr Cys Gln Pro Cys Phe Leu Lys Leu Phe Gly
            435             440             445


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<213> Homo sapien

<400> 4
Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
 1           5               10              15

Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
            20              25              30

Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
        35              40              45

Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser
    50              55              60

Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu
65              70              75              80

Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser
            85              90              95
```

9

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Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln
            100             105             110

Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly
            115             120             125

Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu
    130             135             140

Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser
145             150             155             160

Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro
                165             170             175

Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly
        180             185             190

Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys
        195             200             205

Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr
    210             215             220

Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys
225             230             235             240

Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro
            245             250             255

Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe
        260             265             270

Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His
        275             280             285

Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly
    290             295             300

Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp
305             310             315             320

Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile
            325             330             335

Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys
            340             345             350

Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe
            355             360             365
```

10

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Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg
    370             375             380

Gly Ser Leu Cys Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val
385             390      ·          395             400

Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe
            405             410             415

Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys
        420             425             430

Pro Tyr Cys Gln Pro Cys Phe Leu Lys Leu Phe Gly
    435             440
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<213> Homo sapien

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                           Met Ala Ala Gln Gly Glu Pro Gln Val
                            1               5

cag ttc aaa ctt gta ttg gtt ggt gat ggt ggt act gga aaa acg acc    99
Gln Phe Lys Leu Val Leu Val Gly Asp Gly Gly Thr Gly Lys Thr Thr
10              15              20                      25

ttc gtg aaa cgt cat ttg act ggt gaa ttt gag aag aag tat gta gcc   147
Phe Val Lys Arg His Leu Thr Gly Glu Phe Glu Lys Lys Tyr Val Ala
                30              35              40

acc ttg ggt gtt gag gtt cat ccc cta gtg ttc cac acc aac aga gga   195
Thr Leu Gly Val Glu Val His Pro Leu Val Phe His Thr Asn Arg Gly
            45              50              55
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cct att aag ttc aat gta tgg gac aca gcc ggc cag gag aaa ttc ggt    243
Pro Ile Lys Phe Asn Val Trp Asp Thr Ala Gly Gln Glu Lys Phe Gly
        60                  65                  70

gga ctg aga gat ggc tat tat atc caa gcc cag tgt gcc atc ata atg    291
Gly Leu Arg Asp Gly Tyr Tyr Ile Gln Ala Gln Cys Ala Ile Ile Met
        75                  80                  85

ttt gat gta aca tcg aga gtt act tac aag aat gtg cct aac tgg cat    339
Phe Asp Val Thr Ser Arg Val Thr Tyr Lys Asn Val Pro Asn Trp His
90                  95                  100                 105

aga gat ctg gta cga gtg tgt gaa aac atc ccc att gtg ttg tgt ggc    387
Arg Asp Leu Val Arg Val Cys Glu Asn Ile Pro Ile Val Leu Cys Gly
                110                 115                 120

aac aaa gtg gat att aag gac agg aaa gtg aag gcg aaa tcc att gtc    435
Asn Lys Val Asp Ile Lys Asp Arg Lys Val Lys Ala Lys Ser Ile Val
                125                 130                 135

ttc cac cga aag aag aat ctt cag tac tac gac att tct gcc aaa agt    483
Phe His Arg Lys Lys Asn Leu Gln Tyr Tyr Asp Ile Ser Ala Lys Ser
                140                 145                 150

aac tac aac ttt gaa aag ccc ttc ctc tgg ctt gct agg aag ctc att    531
Asn Tyr Asn Phe Glu Lys Pro Phe Leu Trp Leu Ala Arg Lys Leu Ile
        155                 160                 165

gga gac cct aac ttg gaa ttt gtt gcc atg cct gct ctc gcc cca cca    579
Gly Asp Pro Asn Leu Glu Phe Val Ala Met Pro Ala Leu Ala Pro Pro
170                 175                 180                 185

gaa gtt gtc atg gac cca gct ttg gca gca cag tat gag cac gac tta    627
Glu Val Val Met Asp Pro Ala Leu Ala Ala Gln Tyr Glu His Asp Leu
                190                 195                 200

gag gtt gct cag aca act gct ctc ccg gat gag gat gat gac ctg tga    675
Glu Val Ala Gln Thr Thr Ala Leu Pro Asp Glu Asp Asp Asp Leu
                205                 210                 215

gaatgaagct ggagcccagc gtcagaagtc tagttttata ggcagctgtc ctgtgatgtc    735

agcggtgcag cgtgtgtgcc acctcattat tatctagcta agcggaacat gtgctttatc    795

tgtgggatgc tgaaggagat gagtgggctt cggagtgaat gtggcagttt aaaaaataac    855

ttcattgttt ggacctgcat atttagctgt ttggacgcag ttgattcctt gagtttcata    915

tataagactg ctgcagtcac atcacaatat tcagtggtga aatcttgttt gttactgtca    975

ttcccattcc ttttctttag aatcagaata aagttgtatt tcaaatatct aagcaagtga   1035
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actcatccct tgtttataaa tagcatttgg aaaccactaa agtagggaag ttttatgcca 1095

tgttaatatt tgaattgcct tgcttttatc acttaatttg aaatctattg ggttaatttc 1155

tccctatgtt tattttttgta catttgagcc atgtcacaca aactgatgat gacaggtcag 1215

cagtattcta tttggttaga agggttacat ggtgtaaata ttagtgcagt taagctaaag 1275

cagtgtttgc tccaccttca tattggctag gtagggtcac ctagggaagc acttgctcaa 1335

aatctgtgac ctgtcagaat aaaaatgtgg tttgtacata tcaaatagat attttaaggg 1395

taatattttc ttttatggca aaagtaatca tgttttaatg tagaacctca aacaggatgg 1455

aacatcagtg gatggcagga ggttgggaat tcttgctgtt aaaaataatt acaaattttg 1515

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<210> 6
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<212> PRT
<213> Homo sapien

<400> 6

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Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
            20                  25                  30

Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
        35                  40                  45

Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
    50                  55                  60

Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
65                  70                  75                  80

Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
                85                  90                  95

Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
                100                 105                 110

Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
                115                 120                 125

Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
            130                 135                 140
```

13

```
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145             150             155             160

Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
                165             170             175

Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
            180             185             190

Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
            195             200             205

Leu Pro Asp Glu Asp Asp Asp Leu
    210             215
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<210> 7
<211> 4839
<212> DNA
<213> Homo sapien

<220>
<221> CDS
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<400> 7
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gcgtgccccg cgtgcgcgcg cgtcgtcctc cccggcgctc ctccacagct cgctggctcc 120

cgccgcggaa aggcgtc atg ccg ccc aaa acc ccc cga aaa acg gcc gcc   170
                   Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
                    1               5                   10

acc gcc gcc gct gcc gcc gcg gaa ccc ccg gca ccg ccg ccg ccg ccc  218
Thr Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
                15                  20                  25

cct cct gag gag gac cca gag cag gac agc ggc ccg gag gac ctg cct  266
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
            30                  35                  40

ctc gtc agg ctt gag ttt gaa gaa aca gaa gaa cct gat ttt act gca  314
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
    45                  50                  55

tta tgt cag aaa tta aag ata cca gat cat gtc aga gag aga gct tgg  362
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60                  65                  70                  75
```

```
tta act tgg gag aaa gtt tca tct gtg gat gga gta ttg gga ggt tat    410
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
            80              85              90

att caa aag aaa aag gaa ctg tgg gga atc tgt atc ttt att gca gca    458
Ile Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
            95              100             105

gtt gac cta gat gag atg tcg ttc act ttt act gag cta cag aaa aac    506
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
            110             115             120

ata gaa atc agt gtc cat aaa ttc ttt aac tta cta aaa gaa att gat    554
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
        125             130             135

acc agt acc aaa gtt gat aat gct atg tca aga ctg ttg aag aag tat    602
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
140             145             150             155

gat gta ttg ttt gca ctc ttc agc aaa ttg gaa agg aca tgt gaa ctt    650
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
            160             165             170

ata tat ttg aca caa ccc agc agt tcg ata tct act gaa ata aat tct    698
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
            175             180             185

gca ttg gtg cta aaa gtt tct tgg atc aca ttt tta tta gct aaa ggg    746
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
            190             195             200

gaa gta tta caa atg gaa gat gat ctg gtg att tca ttt cag tta atg    794
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
            205             210             215

cta tgt gtc ctt gac tat ttt att aaa ctc tca cct ccc atg ttg ctc    842
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
220             225             230             235

aaa gaa cca tat aaa aca gct gtt ata ccc att aat ggt tca cct cga    890
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
            240             245             250

aca ccc agg cga ggt cag aac agg agt gca cgg ata gca aaa caa cta    938
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
            255             260             265

gaa aat gat aca aga att att gaa gtt ctc tgt aaa gaa cat gaa tgt    986
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
            270             275             280
```

15

```
aat ata gat gag gtg aaa aat gtt tat ttc aaa aat ttt ata cct ttt      1034
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
    285             290             295

atg aat tct ctt gga ctt gta aca tct aat gga ctt cca gag gtt gaa      1082
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
300             305             310             315

aat ctt tct aaa cga tac gaa gaa att tat ctt aaa aat aaa gat cta      1130
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
            320             325             330

gat gca aga tta ttt ttg gat cat gat aaa act ctt cag act gat tct      1178
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
        335             340             345

ata gac agt ttt gaa aca cag aga aca cca cga aaa agt aac ctt gat      1226
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp
        350             355             360

gaa gag gtg aat gta att cct cca cac act cca gtt agg act gtt atg      1274
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
    365             370             375

aac act atc caa caa tta atg atg att tta aat tca gca agt gat caa      1322
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
380             385             390             395

cct tca gaa aat ctg att tcc tat ttt aac aac tgc aca gtg aat cca      1370
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
            400             405             410

aaa gaa agt ata ctg aaa aga gtg aag gat ata gga tac atc ttt aaa      1418
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys
            415             420             425

gag aaa ttt gct aaa gct gtg gga cag ggt tgt gtc gaa att gga tca      1466
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser
        430             435             440

cag cga tac aaa ctt gga gtt cgc ttg tat tac cga gta atg gaa tcc      1514
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser
    445             450             455

atg ctt aaa tca gaa gaa gaa cga tta tcc att caa aat ttt agc aaa      1562
Met Leu Lys Ser Glu Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys
460             465             470             475

ctt ctg aat gac aac att ttt cat atg tct tta ttg gcg tgc gct ctt      1610
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu
            480             485             490
```

16

```
· gag gtt gta atg gcc aca tat agc aga agt aca tct cag aat ctt gat    1658
  Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp
              495             500             505


  tct gga aca gat ttg tct ttc cca tgg att ctg aat gtg ctt aat tta    1706
  Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu
              510             515             520


  aaa gcc ttt gat ttt tac aaa gtg atc gaa agt ttt atc aaa gca gaa    1754
  Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu
              525             530             535


  ggc aac ttg aca aga gaa atg ata aaa cat tta gaa cga tgt gaa cat    1802
  Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His
  540             545             550             555


  cga atc atg gaa tcc ctt gca tgg ctc tca gat tca cct tta ttt gat    1850
  Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
              560             565             570


  ctt att aaa caa tca aag gac cga gaa gga cca act gat cac ctt gaa    1898
  Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
              575             580             585


  tct gct tgt cct ctt aat ctt cct ctc cag aat aat cac act gca gca    1946
  Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala
              590             595             600


  gat atg tat ctt tct cct gta aga tct cca aag aaa aaa ggt tca act    1994
  Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
  605             610             615


  acg cgt gta aat tct act gca aat gca gag aca caa gca acc tca gcc    2042
  Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala
  620             625             630             635


  ttc cag acc cag aag cca ttg aaa tct acc tct ctt tca ctg ttt tat    2090
  Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
              640             645             650


  aaa aaa gtg tat cgg cta gcc tat ctc cgg cta aat aca ctt tgt gaa    2138
  Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
              655             660             665


  cgc ctt ctg tct gag cac cca gaa tta gaa cat atc atc tgg acc ctt    2186
  Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
              670             675             680


  ttc cag cac acc ctg cag aat gag tat gaa ctc atg aga gac agg cat    2234
  Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
  685             690             695
```

17

```
ttg gac caa att atg atg tgt tcc atg tat ggc ata tgc aaa gtg aag     2282
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
700                     705                 710                 715

aat ata gac ctt aaa ttc aaa atc att gta aca gca tac aag gat ctt     2330
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
                    720                 725                 730

cct cat gct gtt cag gag aca ttc aaa cgt gtt ttg atc aaa gaa gag     2378
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
                735                 740                 745

gag tat gat tct att ata gta ttc tat aac tcg gtc ttc atg cag aga     2426
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg
                750                 755                 760

ctg aaa aca aat att ttg cag tat gct tcc acc agg ccc cct acc ttg     2474
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu
        765                 770                 775

tca cca ata cct cac att cct cga agc cct tac aag ttt cct agt tca     2522
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
780                     785                 790                 795

ccc tta cgg att cct gga ggg aac atc tat att tca ccc ctg aag agt     2570
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
                800                 805                 810

cca tat aaa att tca gaa ggt ctg cca aca cca aca aaa atg act cca     2618
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
                815                 820                 825

aga tca aga atc tta gta tca att ggt gaa tca ttc ggg act tct gag     2666
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
            830                 835                 840

aag ttc cag aaa ata aat cag atg gta tgt aac agc gac cgt gtg ctc     2714
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
        845                 850                 855

aaa aga agt gct gaa gga agc aac cct cct aaa cca ctg aaa aaa cta     2762
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
860                     865                 870                 875

cgc ttt gat att gaa gga tca gat gaa gca gat gga agt aaa cat ctc     2810
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
                880                 885                 890

cca gga gag tcc aaa ttt cag cag aaa ctg gca gaa atg act tct act     2858
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
                895                 900                 905
```

18

```
cga aca cga atg caa aag cag aaa atg aat gat agc atg gat acc tca   2906
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
        910                     915                 920
```

```
aac aag gaa gag aaa tga ggatctcagg accttggtgg acactgtgta          2954
Asn Lys Glu Glu Lys
        925
```

```
cacctctgga ttcattgtct ctcacagatg tgactgtata actttcccag gttctgttta 3014

tggccacatt taatatcttc agctcttttt gtggatataa aatgtgcaga tgcaattgtt 3074

tgggtgattc ctaagccact tgaaatgtta gtcattgtta tttatacaag attgaaaatc 3134

ttgtgtaaat cctgccattt aaaaagttgt agcagattgt ttcctcttcc aaagtaaaat 3194

tgctgtgctt tatggatagt aagaatggcc ctagagtggg agtcctgata acccaggcct 3254

gtctgactac tttgccttct tttgtagcat ataggtgatg tttgctcttg tttttattaa 3314

tttatatgta tattttttta atttaacatg aacacccttа gaaatgtgt cctatctatc 3374

ttccaaatgc aatttgattg actgcccatt caccaaaatt atcctgaact cttctgcaaa 3434

aatggatatt attagaaatt agaaaaaaat tactaatttt acacattaga ttttatttta 3494

ctattggaat ctgatatact gtgtgcttgt tttataaaat tttgctttta attaaataaa 3554

agctggaagc aaagtataac catatgatac tatcatacta ctgaaacaga tttcatacct 3614

cagaatgtaa aagaacttac tgattatttt cttcatccaa cttatgtttt taaatgagga 3674

ttattgatag tactcttggt ttttatacca ttcagatcac tgaatttata aagtacccat 3734

ctagtacttg aaaaagtaaa gtgttctgcc agatcttagg tatagaggac cctaacacag 3794

tatatcccaa gtgcactttc taatgtttct gggtcctgaa gaattaagat acaaattaat 3854

tttactccat aaacagactg ttaattatag gagccttaat ttttttttca tagagatttg 3914

tctaattgca tctcaaaatt attctgccct ccttaatttg ggaaggtttg tgttttctct 3974

ggaatggtac atgtcttcca tgtatctttt gaactggcaa ttgtctattt atcttttatt 4034

tttttaagtc agtatggtct aacactggca tgttcaaagc cacattattt ctagtccaaa 4094

attacaagta atcaagggtc attatgggtt aggcattaat gtttctatct gattttgtgc 4154

aaaagcttca aattaaaaca gctgcattag aaaaagaggc gcttctcccc tccctacac 4214

ctaaaggtgt atttaaacta tcttgtgtga ttaacttatt tagagatgct gtaacttaaa 4274
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19

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ataggggata tttaaggtag cttcagctag cttttaggaa aatcactttg tctaactcag 4334

aattattttt aaaaagaaat ctggtcttgt tagaaaacaa aattttattt tgtgctcatt 4394

taagtttcaa acttactatt ttgacagtta ttttgataac aatgacacta gaaaacttga 4454

ctccatttca tcattgtttc tgcatgaata tcatacaaat cagttagttt ttaggtcaag 4514

ggcttactat ttctgggtct tttgctacta agttcacatt agaattagtg ccagaatttt 4574

aggaacttca gagatcgtgt attgagattt cttaaataat gcttcagata ttattgcttt 4634

attgcttttt tgtattggtt aaaactgtac atttaaaatt gctatgttac tattttctac 4694

aattaatagt ttgtctattt taaaataaat tagttgttaa gagtcttaat ggtctgatgt 4754

tgtgttcttt gtattaagta cactaatgtt ctcttttctg tctaggagaa gatagataga 4814

agataactct cctagtatct catcc                                        4839
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<210> 8
<211> 928
<212> PRT
<213> Homo sapien

<400> 8
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
  1               5                  10                  15

Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp
             20              25              30

Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
         35              40              45

Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
    50              55              60

Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65              70              75              80

Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
                85              90              95

Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
            100             105             110

Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
        115             120             125
```

20

```
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
   130                   135               140

Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145                   150               155                   160

Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
               165               170                   175

Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
           180               185                   190

Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
           195               200               205

Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
   210               215               220

Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225               230               235                   240

Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
               245               250               255

Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
           260               265               270

Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
           275               280               285

Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
   290               295               300

Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305               310               315                   320

Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
               325               330               335

Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
           340               345               350

Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
           355               360               365

Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
   370               375               380

Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385               390               395               400
```

21

```
    Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
                 405             410             415

    Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
                 420             425             430

    Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
                 435             440             445

    Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
             450             455             460

    Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
    465             470             475             480

    Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
                 485             490             495    .

    Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
                 500             505             510

    Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
             515             520             525

    Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
        530             535             540

    Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
    545             550             555             560

    Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
                 565             570             575

    Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
                 580             585             590

    Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
             595             600             605

    Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
        610             615             620

    Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
    625             630             635             640

    Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
                 645             650             655

    Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
                 660             665             670
```

22

```
His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
        675             680              685

Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
    690             695              700

Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705             710              715              720

Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
            725             730              735

Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
        740             745              750

Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
        755             760              765

Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
    770             775              780

Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785             790              795              800

Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
            805             810              815

Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
            820             825              830

Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
        835             840              845

Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
    850             855              860

Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865             870             875              880

Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
            885             890              895

Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
        900             905              910

Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
    915             920              925
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23

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<210> 9
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 9
ttctgtagtt taattttctg aacctttggc                                    30

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      Oligonucleotide

<400> 10
tcagccgaag agcttcagga agcaggg                                       27

<210> 11
<211> 32
<212> PRT
<213> Homo sapien

<220>
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<220>
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<222> (6)..(13)

<220>
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<222> (15)

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<220>
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<222> (20)..(21)
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24

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<222> (23)..(28)

<220>
<221> VARIANT
<222> (30)..(31)

<400> 11
Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa His
 1               5                  10                  15

Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Cys
            20                  25                  30

<210> 12
<211> 50
<212> PRT
<213> Homo sapien

<220>
<221> VARIANT
<222> (2)..(3)

<220>
<221> VARIANT
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<220>
<221> VARIANT
<222> (22)..(23)

<220>
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<222> (25)..(26)

<220>
<221> VARIANT
<222> (28)..(29)

<220>
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<222> (31)..(46)

<220>
<221> VARIANT
<222> (48)..(49)

<400> 12
Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1               5                  10                  15
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```
Xaa Xaa Xaa Xaa His Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa
            20                  25                  30
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa
        35                  40                  45
Xaa Cys
    50
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<210> 13
<211> 1497
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 13
ctgcagcttg ttctttaatg tcaggagact ctcccttctg cttgtcctgg tgggccctgg    60
gggagcgggg gagggaatac ctaagagcaa ttggtagctg gtacttctaa tgcctcttcc   120
tcctccaacc tccaagagtc tgttttggga ttgggttcag gaatgaaatt ctgcctgtgc   180
taacctcctg gggagccggt agacttgtct gttaaaaatc gcttctgctt ttggagccta   240
aagcccggtt ccgaaaaaca agtggtattt aggggaaaga ggggtcttca aaggctacag   300
tgagtcattc cagccttcaa ccatactacg ccagcactac gttctctaaa gccactctgc   360
gctagcttgc ggtgagggga ggggagaaaa ggaaagggga ggggaggggga ggggaggggag   420
aaaggaggtg ggaaggcaga gaggccggct gcggggcggg gaccgactca caaactgttc   480
gatttcgttt ccacctccca gcgccccctc ggagatccct aggagccagc ctgctgggag   540
aaccagaggg tccggagcaa acctggaggc tgagagggca tcagagggga aaagactgag   600
ctagccactc cagtgccata cagaagctta agggacgcac cacgccagcc ccagcccagc   660
gacagccaac gcctgttgca gagcggcggc ttcgaagccg ccgcccagga gctgcccttt   720
cctcttcggt gaagtttcta aaagctgcgg gagactcaga ggaagcaagg aaagtgtccg   780
gtaggactac ggctgccttt gtcctcttcc cctctaccct taccccctcc tgggtcccct   840
ctccaggagc tgactaggca ggctttctgg ccaaccctct cccctacacc cccagctctg   900
ccagccagtt tgcacagagg taaactccct ttggctgaga gtaggggagc ttgttgcaca   960
ttgcaaggaa ggcttttggg agcccagaga ctgaggagca acagcacgcc caggagagtc  1020
cctggttcca ggttctcgcc cctgcacctc ctcctgcccg cccctcaccc tgtgtgtggt  1080
gttagaaatg aaaagatgaa aaggcagcta gggtttcagt agtcgaaagc aaaacaaaag  1140
ctaaaagaaa acaaaaagaa aatagcccag ttcttatttg cacctgcttc agtggacttt  1200
gaatttggaa ggcagaggat ttccccttttt ccctccgtc aaggtttgag catcttttaa  1260
tctgttcttc aagtatttag agacaaactg tgtaagtagc agggcagatc ctgtcttgcg  1320
cgtgccttcc tttactggag actttgaggt tatctgggca ctcccccac ccaccccccc  1380
tcctgcaagt tttcttcccc ggagcttccc gcaggtgggc agctagctgc agatactaca  1440
tcatcagtca ggagaactct tcagagcaag agacgaggag gcaggataag ggaattc     1497
```

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<210> 14
<211> 600
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 14
ctgcagcttg ttctttaatg tcaggagact ctcccttctg cttgtcctgg tgggccctgg    60
gggagcgggg gagggaatac ctaagagcaa ttggtagctg gtacttctaa tgcctcttcc   120
tcctccaacc tccaagagtc tgttttggga ttgggttcag gaatgaaatt ctgcctgtgc   180
taacctcctg gggagccggt agacttgtct gttaaaaatc gcttctgctt ttggagccta   240
aagcccggtt ccgaaaaaca agtggtattt aggggaaaga ggggtcttca aaggctacag   300
tgagtcattc cagccttcaa ccatactacg ccagcactac gttctctaaa gccactctgc   360
gctagcttgc ggtgagggga ggggagaaaa ggaaagggga ggggaggggga ggggaggggag   420
```

```
aaaggaggtg ggaaggcaga gaggccggct gcggggcgg gaccgactca caaactgttc      480
gatttcgttt ccacctccca gcgcccctc ggagatccct aggagccagc ctgctgggag      540
aaccagaggg tccggagcaa acctggaggc tgagagggca tcagagggga aaagactgag      600
```

```
<210> 15
<211> 359
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 15
cccaagcgct agtgttctgt tctctttttg taatcttgga atcttttgtt gctctaaata      60
caattaaaaa tggcagaaac ttgtttgttg gaatacatgt gtgactcttg gtttgtctct      120
gcgtctggct ttagaaatgt catccattgt gtaaatact ggcttgttgg tctgccagct       180
aaaacttgcc acagccctg ttgtgactgc aggctcaagt tattgttaac aaagagcccc        240
aagaaaagct gctaatgtcc tcttatcacc attgttaatt tgttaaaaca taaaacaatc      300
taaaatttca gatgaatgtc atcagagttc ttttcattag ctcttttat tggctgtct        359
```

```
<210> 16
<211> 899
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 16
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1               5                   10                  15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
            20                  25                  30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
        35                  40                  45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
    50                  55                  60
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
65                  70                  75                  80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
                85                  90                  95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
            100                 105                 110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
        115                 120                 125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
    130                 135                 140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145                 150                 155                 160
Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
                165                 170                 175
Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln
            180                 185                 190
Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
        195                 200                 205
Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr
    210                 215                 220
Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met
225                 230                 235                 240
```

27

```
Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu
            245                 250                 255
Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val
            260                 265                 270
Arg Pro Thr Pro Cys Ala Pro Leu Pro Glu Cys Lys Gly Leu Pro Leu
            275                 280                 285
Asp Glu Gly Pro Gly Lys Ser Thr Glu Glu Thr Ala Glu Tyr Ser Ser
    290                 295                 300
Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys
305                 310                 315                 320
Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu Ile Pro Ser
            325                 330                 335
Ser Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr
            340                 345                 350
Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser Gly Pro Pro
            355                 360                 365
His Pro Pro Pro Pro Thr His Pro His Ala Arg Ile Lys Leu Glu Asn
    370                 375                 380
Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg
385                 390                 395                 400
Tyr Gly Asp Leu Gly Ser Leu His Gly Gly Ser Val Ala Gly Pro Ser
            405                 410                 415
Thr Gly Ser Pro Pro Ala Thr Thr Ser Ser Ser Trp His Thr Leu Phe
            420                 425                 430
Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly Gly Gly Ser
            435                 440                 445
Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly Tyr Thr Arg
    450                 455                 460
Pro Pro Gln Gly Leu Thr Ser Gln Glu Ser Asp Tyr Ser Ala Ser Glu
465                 470                 475                 480
Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr Pro Ser Pro
            485                 490                 495
Asn Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn Tyr Ser Gly
            500                 505                 510
Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
            515                 520                 525
Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
    530                 535                 540
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545                 550                 555                 560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
            565                 570                 575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
            580                 585                 590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
            595                 600                 605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
    610                 615                 620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625                 630                 635                 640
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
            645                 650                 655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
            660                 665                 670
Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
            675                 680                 685
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
    690                 695                 700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705                 710                 715                 720
```

```
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
                725                 730                 735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
        740                 745                 750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
        755                 760                 765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
    770                 775                 780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785                 790                 795                 800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
                805                 810                 815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
                820                 825                 830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
        835                 840                 845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
    850                 855                 860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
865                 870                 875                 880
Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
                885                 890                 895
His Thr Gln
```

```
<210> 17
<211> 2988
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 17
gcttcccgca ggtgggcagc tagctgcaga tactacatca tcagtcagga gaactcttca      60
gagcaagaga cgaggaggca ggataaggga attcggtgga agctacagac aagctcaagg     120
atggaggtgc agttagggct gggaagggtc tacccacggc ccccatccaa gacctatcga     180
ggagcgttcc agaatctgtt ccagagcgtg cgcgaagcga tccagaaccc gggcccccagg    240
caccctgagg ccgctaacat agcacctccc ggcgcctgtt tacagcagag gcaggagact     300
agcccccggc ggcggcggcg gcagcagcac actgaggatg gttctcctca gcccacatc      360
agaggcccca caggctacct ggccctggag gaggaacagc agccttcaca gcagcaggca     420
gcctccgagg gccacccctga gagcagctgc ctccccgagc ctggggcggc caccgctcct    480
ggcaagggc tgccgcagca gccaccagct cctccagatc aggatgactc agctgccca      540
tccacgttgt ccctgctggg ccccactttc ccaggcttaa gcagctgctc cgccgacatt     600
aaagacattt tgaacgaggc cggcaccatg caacttcttc agcagcagca acaacagcag     660
cagcaccaac agcagcacca acagcaccaa cagcagcagg aggtaatctc cgaaggcagc     720
agcgcaagag ccaggaggc cacggggggct ccctcttcct ccaaggatag ttacctaggg    780
ggcaattcaa ccatatctga cagtgccaag gagttgtgta agcagtgtc tgtgtccatg      840
ggattgggtg tggaagcatt ggaacatctg agtccagggg aacagcttcg gggagactgc     900
atgtacgcgt cgctcctggg aggtccaccc gcggtgcgtc ccactccttg tgcgccgctg     960
cccgaatgca aaggtcttcc cctggacgaa ggcccaggca aaagcactga agagactgct    1020
gagtattcct ctttcaaggg aggttacgcc aaaggattgg aaggtgagag cttggggtgc    1080
tctggcagca gtgaagcagg tagctctggg acacttgaga tcccgtcctc tctgtctctg    1140
tataaatctg gagcactaga cgaggcagca gcataccaga atcgcgacta ctacaacttt    1200
ccgctggctc tgtccgggcc gccgcacccc ccgccccctca cccatccaca cgcccgtatc    1260
aagctggaga acccattgga ctacggcagc gcctgggctg cggcggcagc gcaatgccgc    1320
tatggggact tgggtagtct acatggaggg agtgtagccg ggcccagcac tggatcgccc    1380
ccagccacca cctcttcttc ctggcatact ctcttcacag ctgaagaagg ccaattatat    1440
gggccaggag gcggggcgg cagcagcagc ccaagcgatg ccgggcctgt agcccctat     1500
ggctacactc ggcccctca ggggctgaca agccaggaga gtgactactc tgcctccgaa     1560
```

```
gtgtggtatc ctggtggagt tgtgaacaga gtaccctatc ccagtcccaa ttgtgtcaaa    1620
agtgaaatgg gaccttggat ggagaactac tccggacctt atggggacat gcgtttggac    1680
agtaccaggg accatgtttt acccatcgac tattactttc cacccagaa gacctgcctg      1740
atctgtggag atgaagcttc tggctgtcac tacggagctc tcacttgtgg cagctgcaag    1800
gtcttcttca aaagagccgc tgaagggaaa cagaagtatc tatgtgccag cagaaacgat    1860
tgtaccattg ataaatttcg gaggaaaaat tgcccatctt gtcgtctccg gaaatgttat    1920
gaagcaggga tgactctggg agctcgtaag ctgaagaaac ttggaaatct aaaactacag    1980
gaggaaggag aaaactccaa tgctggcagc cccactgagg acccatccca gaagatgact    2040
gtatcacaca ttgaaggcta tgaatgtcag cctatctttc ttaacgtcct ggaagccatt    2100
gagccaggag tggtgtgtgc cggacatgac aacaaccaac cagattcctt tgctgccttg    2160
ttatctagcc tcaatgagct tggagagagg cagcttgtgc atgtggtcaa gtgggccaag    2220
gccttgcctg gcttccgcaa cttgcatgtg gatgaccaga tggcggtcat tcagtattcc    2280
tggatgggac tgatggtatt tgccatgggt tggcggtcct tcactaatgt caactccagg    2340
atgctctact ttgcacctga cttggttttc aatgagtacc gcatgcacaa gtctcggatg    2400
tacagccagt gtgtgaggat gaggcacctg tctcaagagt ttggatggct ccaaataacc    2460
ccccaggaat tcctgtgcat gaaagcactg ctgctcttca gcattattcc agtggatggg    2520
ctgaaaaatc aaaaattctt tgatgaactt cgaatgaact acatcaagga actcgatcgc    2580
atcattgcat gcaaaagaaa gaatcccaca tcctgctcaa ggcgcttcta ccagctcacc    2640
aagctcctgg attctgtgca gcctattgca agagagctgc atcagttcac ttttgacctg    2700
ctaatcaagt cccatatggt gagcgtggac tttcctgaaa tgatggcaga gatcatctct    2760
gtgcaagtgc ccaagatcct ttctgggaaa gtcaagccca tctatttcca cacacagtga    2820
agatttggaa accctaatac ccaaaaccca ccttgttccc tttccagatg tcttctgcct    2880
gttatataac tctgcactac ttctctgcag tgccttgggg gaaattcctc tactgatgta    2940
cagtcagacg tgaacaggtt cctcagttct atttcctggg cttctcct              2988
```

```
<210> 18
<211> 899
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 18
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1               5                   10                  15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
            20                  25                  30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
        35                  40                  45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
    50                  55                  60
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
65                  70                  75                  80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Gln Gln Pro Ser
            85                  90                  95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
            100                 105                 110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
        115                 120                 125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
    130                 135                 140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145                 150                 155                 160
Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
            165                 170                 175
Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln
            180                 185                 190
Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
        195                 200                 205
```

```
Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr
    210                 215                 220
Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met
225                 230                 235                 240
Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu
            245                 250                 255
Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val
            260                 265                 270
Arg Pro Thr Pro Cys Ala Pro Leu Pro Glu Cys Lys Gly Leu Pro Leu
        275                 280                 285
Asp Glu Gly Pro Gly Lys Ser Thr Glu Glu Thr Ala Glu Tyr Ser Ser
    290                 295                 300
Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys
305                 310                 315                 320
Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu Ile Pro Ser
            325                 330                 335
Ser Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr
        340                 345                 350
Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser Gly Pro Pro
        355                 360                 365
His Pro Pro Pro Thr His Pro His Ala Arg Ile Lys Leu Glu Asn
    370                 375                 380
Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg
385                 390                 395                 400
Tyr Gly Asp Leu Gly Ser Leu His Gly Gly Ser Val Ala Gly Pro Ser
            405                 410                 415
Thr Gly Ser Pro Pro Ala Thr Thr Ser Ser Ser Trp His Thr Leu Phe
            420                 425                 430
Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly Gly Gly Ser
        435                 440                 445
Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly Tyr Thr Arg
    450                 455                 460
Pro Pro Gln Gly Leu Thr Ser Gln Glu Ser Asp Tyr Ser Ala Ser Glu
465                 470                 475                 480
Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr Pro Ser Pro
            485                 490                 495
Asn Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn Tyr Ser Gly
        500                 505                 510
Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
        515                 520                 525
Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
    530                 535                 540
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545                 550                 555                 560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
            565                 570                 575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
        580                 585                 590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
        595                 600                 605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
    610                 615                 620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625                 630                 635                 640
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
            645                 650                 655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
            660                 665                 670
Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
    675                 680                 685
```

31

```
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
    690                 695             700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705                 710             715                 720
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
            725             730                 735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
            740             745                 750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
    755             760             765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
    770             775             780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785             790             795                 800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
            805             810             815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
            820             825             830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
    835             840             845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
    850             855             860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
865             870             875                 880
Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
            885             890             895
His Thr Gln
```

```
<210> 19
<211> 2988
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 19
gcttcccgca ggtgggcagc tagctgcaga tactacatca tcagtcagga gaactcttca    60
gagcaagaga cgaggaggca ggataaggga attcggtgga agctacagac aagctcaagg   120
atggaggtgc agttagggct gggaagggtc tacccacggc ccccatccaa gacctatcga   180
ggagcgttcc agaatctgtt ccagagcgtg cgcgaagcga tccagaaccc gggccccagg   240
caccctgagg ccgctaacat agcacctccc ggcgcctgtt tacagcagag gcaggagact   300
agcccccggc ggcggcggcg gcagcagcac actgaggatg gttctcctca gcccacatc    360
agaggcccca caggctacct ggccctggag gaggaacagc agccttcaca gcagcaggca   420
gcctccgagg gccaccctga gagcagctgc ctccccgagc ctgggcggc caccgctcct    480
ggcaaggggc tgccgcagca gccaccagct cctccagatc aggatgactc agctgcccca   540
tccacgttgt ccctgctggg ccccactttc ccaggcttaa gcagctgctc cgccgacatt   600
aaagacattt tgaacgaggc cggcaccatg caacttcttc agcagcagca acaacagcag   660
cagcaccaac agcagcacca acagcaccaa cagcagcagg aggtaatctc cgaaggcagc   720
agcgcaagag ccagggaggc cacggggggct ccctcttcct ccaaggatag ttacctaggg   780
ggcaattcaa ccatatctga cagtgccaag gagttgtgta agcagtgtc tgtgtccatg    840
ggattgggtg tggaagcatt ggaacatctg agtccagggg aacagcttcg gggagactgc   900
atgtacgcgt cgctcctggg aggtccaccc gcggtgcgtc ccactccttg tgcgccgctg   960
cccgaatgca aaggtcttcc cctggacgaa ggcccaggca aaagcactga agagactgct  1020
gagtattcct ctttcaaggg aggttacgcc aaaggattgg aaggtgagag cttggggtgc  1080
tctggcagca gtgaagcagg tagctctggg acacttgaga tcccgtcctc tctgtctctg  1140
tataaatctg gagcactaga cgaggcagca gcataccaga atcgcgacta ctacaacttt  1200
ccgctggctc tgtccgggcc gccgcacccc ccgcccccta cccatccaca cgcccgtatc  1260
```

32

```
aagctggaga aacccattgga ctacggcagc gcctgggctg cggcggcagc gcaatgccgc    1320
tatggggact tgggtagtct acatggaggg agtgtagccg ggcccagcac tggatcgccc    1380
ccagccacca cctcttcttc ctggcatact ctcttcacag ctgaagaagg ccaattatat    1440
gggccaggag gcgggggcgg cagcagcagc ccaagcgatg ccgggcctgt agccccctat    1500
ggctacactc ggccccctca ggggctgaca agccaggaga gtgactactc tgcctccgaa    1560
gtgtggtatc ctggtggagt tgtgaacaga gtaccctatc ccagtcccaa ttgtgtcaaa    1620
agtgaaatgg gaccttggat ggagaactac tccggacctt atggggacat gcgtttggac    1680
agtaccaggg accatgtttt acccatcgac tattactttc caccccagaa gacctgcctg    1740
atctgtggag atgaagcttc tggctgtcac tacggagctc tcacttgtgg cagctgcaag    1800
gtcttcttca aaagagccgc tgaagggaaa cagaagtatc tatgtgccag cagaaacgat    1860
tgtaccattg ataaatttcg gaggaaaaat tgcccatctt gtcgtctccg gaaatgttat    1920
gaagcaggga tgactctggg agctcgtaag ctgaagaaac ttggaaatct aaaactacag    1980
gaggaaggag aaaactccaa tgctggcagc cccactgagg acccatccca gaagatgact    2040
gtatcacaca ttgaaggcta tgaatgtcag cctatctttc ttaacgtcct ggaagccatt    2100
gagccaggag tggtgtgtgc cggacatgac aacaaccaac cagattcctt tgctgccttg    2160
ttatctagcc tcaatgagct tggagagagg cagcttgtgc atgtggtcaa gtgggccaag    2220
gccttgcctg cttccgcaa cttgcatgtg gatgaccaga tggcggtcat tcagtattcc    2280
tggatgggac tgatggtatt tgccatgggt tggcggtcct tcactaatgt caactccagg    2340
atgctctact ttgcacctga cttggttttc aatgagtacc gcatgcacaa gtctcggatg    2400
tacagccagt gtgtgaggat gaggcacctg tctcaagagt ttggatggct ccaaataacc    2460
ccccaggaat tcctgtgcat gaaagcactg ctgctcttca gcattattcc agtggatggg    2520
ctgaaaaatc aaaaattctt tgatgaactt cgaatgaact acatcaagga actcgatcgc    2580
atcattgcat gcaaaagaaa gaatcccaca tcctgctcaa ggcgcttcta ccagctcacc    2640
aagctcctgg attctgtgca gcctattgca agagagctgc atcagttcac ttttgacctg    2700
ctaatcaagt cccatatggt gagcgtggac tttcctgaaa tgatggcaga gatcatctct    2760
gtgcaagtgc ccaagatcct ttctgggaaa gtcaagccca tctatttcca cacacagtga    2820
agatttggaa accctaatac ccaaaaccca ccttgttccc tttccagatg tcttctgcct    2880
gttatataac tctgcactac ttctctgcag tgccttgggg gaaattcctc tactgatgta    2940
cagtcagacg tgaacaggtt cctcagttct atttcctggg cttctcct                 2988
```

<210> 20
<211> 899
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 20

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Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1               5                   10                  15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
            20                  25                  30
Ala Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Asn Ile Ala
        35                  40                  45
Pro Pro Gly Ala Cys Leu Gln Gln Arg Gln Glu Thr Ser Pro Arg Arg
    50                  55                  60
Arg Arg Arg Gln Gln His Thr Glu Asp Gly Ser Pro Gln Ala His Ile
65                  70                  75                  80
Arg Gly Pro Thr Gly Tyr Leu Ala Leu Glu Glu Glu Gln Gln Pro Ser
                85                  90                  95
Gln Gln Gln Ala Ala Ser Glu Gly His Pro Glu Ser Ser Cys Leu Pro
            100                 105                 110
Glu Pro Gly Ala Ala Thr Ala Pro Gly Lys Gly Leu Pro Gln Gln Pro
            115                 120                 125
Pro Ala Pro Pro Asp Gln Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser
    130                 135                 140
Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Ile
145                 150                 155                 160
```

33

```
Lys Asp Ile Leu Asn Glu Ala Gly Thr Met Gln Leu Leu Gln Gln Gln
            165                     170                 175
Gln Gln Gln Gln Gln His Gln Gln Gln His Gln Gln His Gln Gln Gln
            180                     185                 190
Gln Glu Val Ile Ser Glu Gly Ser Ser Ala Arg Ala Arg Glu Ala Thr
            195                     200                 205
Gly Ala Pro Ser Ser Ser Lys Asp Ser Tyr Leu Gly Gly Asn Ser Thr
    210                     215                 220
Ile Ser Asp Ser Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser Met
225                     230                 235                 240
Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln Leu
                245                 250                 255
Arg Gly Asp Cys Met Tyr Ala Ser Leu Leu Gly Gly Pro Pro Ala Val
            260             .       265                 270
Arg Pro Thr Pro Cys Ala Pro Leu Pro Glu Cys Lys Gly Leu Pro Leu
        275                     280                 285
Asp Glu Gly Pro Gly Lys Ser Thr Glu Glu Thr Ala Glu Tyr Ser Ser
    290                     295                 300
Phe Lys Gly Gly Tyr Ala Lys Gly Leu Glu Gly Glu Ser Leu Gly Cys
305                     310                 315                 320
Ser Gly Ser Ser Glu Ala Gly Ser Ser Gly Thr Leu Glu Ile Pro Ser
                325                 330                 335
Ser Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala Tyr
            340                     345                 350
Gln Asn Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ser Gly Pro Pro
            355                     360                 365
His Pro Pro Pro Pro Thr His Pro His Ala| Arg Ile Lys Leu Glu Asn
    370                     375                 380
Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala Gln Cys Arg
385                     390                 395                 400
Tyr Gly Asp Leu Gly Ser Leu His Gly Gly Ser Val Ala Gly Pro Ser
                405                 410                 415
Thr Gly Ser Pro Pro Ala Thr Thr Ser Ser Ser Trp His Thr Leu Phe
            420                     425                 430
Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Gly Gly Gly Gly Gly Ser
        435                     440                 445
Ser Ser Pro Ser Asp Ala Gly Pro Val Ala Pro Tyr Gly Tyr Thr Arg
    450                     455                 460
Pro Pro Gln Gly Leu Thr Ser Gln Glu Ser Asp Tyr Ser Ala Ser Glu
465                     470                 475                 480
Val Trp Tyr Pro Gly Gly Val Val Asn Arg Val Pro Tyr Pro Ser Pro
                485                 490                 495
Asn Cys Val Lys Ser Glu Met Gly Pro Trp Met Glu Asn Tyr Ser Gly
            500                     505                 510
Pro Tyr Gly Asp Met Arg Leu Asp Ser Thr Arg Asp His Val Leu Pro
            515                     520                 525
Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly Asp
    530                     535                 540
Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys Lys
545                     550                 555                 560
Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys Ala
                565                 570                 575
Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys Pro
            580                     585                 590
Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly Ala
            595                     600                 605
Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly Glu
    610                     615                 620
Asn Ser Asn Ala Gly Ser Pro Thr Glu Asp Pro Ser Gln Lys Met Thr
625                     630                 635                 640
```

```
Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn Val
            645                 650                 655
Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn Asn
            660                 665                 670
Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu Gly
        675                 680                 685
Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro Gly
    690                 695                 700
Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr Ser
705                 710                 715                 720
Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr Asn
            725                 730                 735
Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn Glu
            740                 745                 750
Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met Arg
        755                 760                 765
His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu Phe
    770                 775                 780
Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro Val Asp Gly
785                 790                 795                 800
Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile Lys
            805                 810                 815
Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser Cys
            820                 825                 830
Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln Pro
        835                 840                 845
Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys Ser
    850                 855                 860
His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile Ser
865                 870                 875                 880
Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr Phe
            885                 890                 895
His Thr Gln
```

<210> 21
<211> 2700
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

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<400> 21
atggaggtgc agttagggct gggaagggtc tacccacggc ccccatccaa gacctatcga     60
ggagcgttcc agaatctgtt ccagagcgtg cgcgaagcga tccagaaccc gggccccagg    120
caccctgagg ccgctaacat agcacctccc ggcgcctgtt tacagcagag gcaggagact    180
agcccccggc ggcggcggcg gcagcagcac actgaggatg gttctcctca gcccacatc    240
agaggcccca caggctacct ggccctggag gaggaacagc agccttcaca gcagcaggca    300
gcctccgagg gccaccctga gagcagctgc ctccccgagc ctggggcggc caccgctcct    360
ggcaaggggc tgccgcagca gccaccagct cctccagatc aggatgactc agctgcccca    420
tccacgttgt ccctgctggg ccccactttc ccaggcttaa gcagctgctc cgccgacatt    480
aaagacattt tgaacgaggc cggcaccatg caacttcttc agcagcagca acaacagcag    540
cagcaccaac agcagcacca acagcaccaa cagcagcagg aggtaatctc cgaaggcagc    600
agcgcaagag ccagggaggc cacggggggct ccctcttcct ccaaggatag ttacctaggg    660
ggcaattcaa ccatatctga cagtgccaag gagttgtgta aagcagtgtc tgtgtccatg    720
ggattgggtg tggaagcatt ggaacatctg agtccagggg aacagcttcg gggagactgc    780
atgtacgcgt cgctcctggg aggtccaccc gcggtgcgtc ccactccttg tgcgccgctg    840
cccgaatgca aaggtcttcc cctggacgaa ggcccaggca aaagcactga gagagactgct    900
gagtattcct ctttcaaggg aggttacgcc aaaggattgg aaggtgagag cttgggggtgc    960
```

35

```
tctggcagca gtgaagcagg tagctctggg acacttgaga tcccgtcctc tctgtctctg    1020
tataaatctg gagcactaga cgaggcagca gcataccaga atcgcgacta ctacaacttt    1080
ccgctggctc tgtccgggcc gccgcacccc ccgcccccta cccatccaca cgcccgtatc    1140
aagctggaga acccattgga ctacggcagc gcctgggctg cggcggcagc gcaatgccgc    1200
tatggggact tgggtagtct acatggaggg agtgtagccg ggcccagcac tggatcgccc    1260
ccagccacca cctcttcttc ctggcatact ctcttcacag ctgaagaagg ccaattatat    1320
gggccaggag gcgggggcgg cagcagcagc ccaagcgatg ccgggcctgt agcccctat     1380
ggctacactc ggcccctca ggggctgaca agccaggaga gtgactactc tgcctccgaa    1440
gtgtggtacc ctggtggagt tgtgaacaga gtaccctatc ccagtcccaa ttgtgtcaaa    1500
agtgaaatgg gaccttggat ggagaactac tccggacctt atggggacat gcgtttggac    1560
agtaccaggg accatgtttt acccatcgac tattactttc caccccagaa gacctgcctg    1620
atctgtggag atgaagcttc tggctgtcac tacggagctc tcacttgtgg cagctgcaag    1680
gtcttcttca aaagagccgc tgaagggaaa cagaagtatc tatgtgccag cagaaacgat    1740
tgtaccattg ataaatttcg gaggaaaaat tgcccatctt gtcgtctccg gaaatgttat    1800
gaagcaggga tgactctggg agctcgtaag ctgaagaaac ttggaaatct aaaactacag    1860
gaggaaggag aaaactccaa tgctggcagc cccactgagg acccatccca gaagatgact    1920
gtatcacaca ttgaaggcta tgaatgtcag cctatctttc ttaacgtcct ggaagccatt    1980
gagccaggag tggtgtgtgc cggacatgac aacaaccaac cagattcctt tgctgccttg    2040
ttatctagcc tcaatgagct tggagagagg cagcttgtgc atgtggtcaa gtgggccaag    2100
gccttgcctg gcttccgcaa cttgcatgtg gatgaccaga tggcggtcat tcagtattcc    2160
tggatgggac tgatggtatt tgccatgggt tggcggtcct tcactaatgt caactccagg    2220
atgctctact ttgcacctga cttggttttc aatgagtacc gcatgcacaa gtctcggatg    2280
tacagccagt gtgtgaggat gaggcacctg tctcaagagt ttggatggct ccaaataacc    2340
ccccaggaat tcctgtgcat gaaagcactg ctgctcttca gcattattcc agtggatggg    2400
ctgaaaaatc aaaaattctt tgatgaactt cgaatgaact acatcaagga actcgatcgc    2460
atcattgcat gcaaaagaaa gaatcccaca tcctgctcaa ggcgcttcta ccagctcacc    2520
aagctcctgg attctgtgca gcctattgca agagagctgc atcagttcac ttttgacctg    2580
ctaatcaagt cccatatggt gagcgtggac tttcctgaaa tgatggcaga gatcatctct    2640
gtgcaagtgc ccaagatcct ttctgggaaa gtcaagccca tctatttcca cacacagtga    2700
```

```
<210> 22
<211> 4321
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 22
cgagatcccg gggagccagc ttgctgggag agcgggacgg tccggagcaa gcccacaggc      60
agaggaggcg acagagggaa aaagggccga gctagccgct ccagtgctgt acaggagccg     120
aagggacgca ccacgccagc cccagcccgg ctccagcgac agccaacgcc tcttgcagcg     180
cggcggcttc gaagccgccg cccggagctg ccctttcctc ttcggtgaag tttttaaaag     240
ctgctaaaga ctcggaggaa gcaaggaaag tgcctggtag gactgacggc tgcctttgtc     300
ctcctcctct ccaccccgcc tcccccacc ctgccttccc ccctccccc gtcttctctc       360
ccgcagctgc ctcagtcggc tactctcagc caaccccct caccacctt ctccccaccc       420
gcccccccgc ccccgtcggc ccagcgctgc cagcccgagt ttgcagagag gtaactccct     480
ttggctgcga gcgggcgagc tagctgcaca ttgcaaagaa ggctcttagg agccaggcga     540
ctggggagcg gcttcagcac tgcagccacg acccgcctgg ttagaattcc ggcggagaga     600
accctctgtt ttcccccact ctctctccac ctcctcctgc cttccccacc ccgagtgcgg     660
agcagagatc aaaagatgaa aaggcagtca ggtcttcagt agccaaaaaa caaaacaaac     720
aaaaacaaaa aagccgaaat aaaagaaaaa gataataact cagttcttat ttgcacctac     780
ttcagtggac actgaatttg gaaggtggag gattttgttt ttttctttta agatctgggc     840
atcttttgaa tctacccttc aagtattaag agacagactg tgagcctagc agggcagatc     900
ttgtccaccg tgtgtcttct tctgcacgag actttgaggc tgtcagagcg cttttttgcgt    960
ggttgctccc gcaagtttcc ttctctggag cttcccgcag gtgggcagct agctgcagcg    1020
actaccgcat catcacagcc tgttgaactc ttctgagcaa gagaagggga ggcggggtaa    1080
gggaagtagg tggaagattc agccaagctc aaggatggaa gtgcagttag ggctgggaag    1140
ggtctaccct cggccgccgt ccaagaccta ccgaggagct ttccagaatc tgttccagag    1200
cgtgcgcgaa gtgatccaga acccgggccc caggcaccca gaggccgcga gcgcagcacc    1260
```

```
tcccggcgcc agtttgctgc tgctgcagca gcagcagcag cagcagcagc agcagcagca   1320
gcagcagcag cagcagcagc agcagcaaga gactagcccc aggcagcagc agcagcagca   1380
gggtgaggat ggttctcccc aagcccatcg tagaggcccc acaggctacc tggtcctgga   1440
tgaggaacag caaccttcac agccgcagtc ggccctggag tgccaccccg agagaggttg   1500
cgtcccagag cctggagccg ccgtggccgc cagcaagggg ctgccgcagc agctgccagc   1560
acctccggac gaggatgact cagctgcccc atccacgttg tccctgctgg gccccacttt   1620
ccccggctta agcagctgct ccgctgacct taaagacatc ctgagcgagg ccagcaccat   1680
gcaactcctt cagcaacagc agcaggaagc agtatccgaa ggcagcagca gcgggagagc   1740
gagggaggcc tcgggggctc ccacttcctc caaggacaat tacttagggg gcacttcgac   1800
catttctgac aacgccaagg agttgtgtaa ggcagtgtcg gtgtccatgg gcctgggtgt   1860
ggaggcgttg gagcatctga gtccagggga acagcttcgg ggggattgca tgtacgcccc   1920
acttttggga gttccacccg ctgtgcgtcc cactccttgt gccccattgg ccgaatgcaa   1980
aggttctctg ctagacgaca gcgcaggcaa gagcactgaa gatactgctg agtattcccc   2040
tttcaaggga ggttacacca aagggctaga aggcgagagc ctaggctgct ctggcagcgc   2100
tgcagcaggg agctccggga cacttgaact gccgtctacc ctgtctctct acaagtccgg   2160
agcactggac gaggcagctg cgtaccagag tcgcgactac tacaactttc cactggctct   2220
ggccggaccg ccgccccctc cgccgcctcc ccatccccac gctcgcatca agctggagaa   2280
cccgctggac tacggcagcg cctgggcggc tgcggcggcg cagtgccgct atggggacct   2340
ggcgagcctg catggcgcgg gtgcagcggg acccggttct gggtcaccct cagccgccgc   2400
ttcctcatcc tggcacactc tcttcacagc cgaagaaggc cagttgtatg accgtgtgg   2460
tggtggtggg ggtggtggcg gcggcggcgg cggcggcggc ggcggcggcg cggcggcgg   2520
cggcggcggc gaggcgggag ctgtagcccc ctacggctac actcggcccc ctcagggct   2580
ggcgggccag gaaagcgact tcaccgcacc tgatgtgtgg taccctggcg gcatggtgag   2640
cagagtgccc tatcccagtc ccacttgtgt caaaagcgaa atgggcccct ggatggatag   2700
ctactccgga ccttacgggg acatgcgttt ggagactgcc aggaccatg ttttgcccat   2760
tgactattac tttccacccc agaagacctg cctgatctgt ggagatgaag cttctgggtg   2820
tcactatgga gctctcacat gtggaagctg caaggtcttc ttcaaaagag ccgctgaagg   2880
gaaacagaag tacctgtgcg ccagcagaaa tgattgcact attgataaat tccgaaggaa   2940
aaattgtcca tcttgtcgtc ttcggaaatg ttatgaagca gggatgactc tgggagcccg   3000
gaagctgaag aaacttggta atctgaaact acaggaggaa ggagaggctt ccagcaccac   3060
cagccccact gaggagacaa cccagaagct gacagtgtca cacattgaag ctatgaatg   3120
tcagcccatc tttctgaatg tcctggaagc cattgagcca ggtgtagtgt gtgctggaca   3180
cgacaacaac cagcccgact cctttgcagc cttgctctct agcctcaatg aactgggaga   3240
gagacagctt gtacacgtgg tcaagtgggc caaggccttg cctggcttcc gcaacttaca   3300
cgtggacgac cagatggctg tcattcagta ctcctggatg gggctcatgg tgtttgccat   3360
gggctggcga tccttcacca atgtcaactc caggatgctc tacttcgccc ctgatctggt   3420
tttcaatgag taccgcatgc acaagtcccg gatgtacagc cagtgtgtcc gaatgaggca   3480
cctctctcaa gagtttggat ggctccaaat cacccccag gaattcctgt gcatgaaagc   3540
actgctactc ttcagcatta ttccagtgga tgggctgaaa aatcaaaaat tctttgatga   3600
acttcgaatg aactacatca aggaactcga tcgtatcatt gcatgcaaaa gaaaaaatcc   3660
cacatcctgc tcaagacgct tctaccagct caccaagctc ctggactccg tgcagcctat   3720
tgcgagagag ctgcatcagt tcacttttga cctgctaatc aagtcacaca tggtgagcgt   3780
ggactttccg gaaatgatgg cagagatcat ctctgtgcaa gtgcccaaga tcctttctgg   3840
gaaagtcaag cccatctatt ccacaccca gtgaagcatt ggaaaccta tttccccacc   3900
ccagctcatg ccccctttca gatgtcttct gcctgttata actctgcact actcctctgc   3960
agtgccttgg ggaatttcct ctattgatgt acagtctgtc atgaacatgt tcctgaattc   4020
tatttgctgg gcttttttt tctctttctc tcctttcttt ttcttcttcc ctccctatct   4080
aaccctccca tggcaccttc agactttgct tcccattgtg gctcctatct gtgttttgaa   4140
tggtgttgta tgcctttaaa tctgtgatga tcctcatatg cccagtgtc aagttgtgct   4200
tgtttacagc actactctgt gccagccaca caaacgttta cttatcttat gccacgggaa   4260
gtttagagag ctaagattat ctggggaaat caaaacaaaa aacaagcaaa caaaaaaaaa   4320
a                                                                   4321
```

```
<210> 23
<211> 919
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct
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<400> 23
Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser
1             5                 10                15
Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu
            20                25                30
Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala
        35                40                45
Pro Pro Gly Ala Ser Leu Leu Leu Leu Gln Gln Gln Gln Gln Gln Gln
    50                55                60
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr
65                70                75                80
Ser Pro Arg Gln Gln Gln Gln Gln Gln Gly Glu Asp Gly Ser Pro Gln
            85                90                95
Ala His Arg Arg Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln
            100               105               110
Gln Pro Ser Gln Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly
        115               120               125
Cys Val Pro Glu Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro
    130               135               140
Gln Gln Leu Pro Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser
145               150               155               160
Thr Leu Ser Leu Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser
            165               170               175
Ala Asp Leu Lys Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu
            180               185               190
Gln Gln Gln Gln Gln Glu Ala Val Ser Glu Gly Ser Ser Ser Gly Arg
            195               200               205
Ala Arg Glu Ala Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu
    210               215               220
Gly Gly Thr Ser Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala
225               230               235               240
Val Ser Val Ser Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser
            245               250               255
Pro Gly Glu Gln Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly
            260               265               270
Val Pro Pro Ala Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys
    275               280               285
Lys Gly Ser Leu Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr
    290               295               300
Ala Glu Tyr Ser Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly
305               310               315               320
Glu Ser Leu Gly Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr
            325               330               335
Leu Glu Leu Pro Ser Thr Leu Ser Leu Tyr Lys Ser Gly Ala Leu Asp
            340               345               350
Glu Ala Ala Ala Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala
    355               360               365
Leu Ala Gly Pro Pro Pro Pro Pro Pro His Pro His Ala Arg
    370               375               380
Ile Lys Leu Glu Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala
385               390               395               400
Ala Ala Gln Cys Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly
            405               410               415
Ala Ala Gly Pro Gly Ser Gly Ser Pro Ser Ala Ala Ser Ser Ser
            420               425               430
Trp His Thr Leu Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys
    435               440               445
Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
    450               455               460
```

```
Gly Gly Gly Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro Tyr
465             470                 475                 480
Gly Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe
            485             490                 495
Thr Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro
        500             505                 510
Tyr Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp
        515             520                 525
Ser Tyr Ser Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg Asp
    530             535                 540
His Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu
545             550                 555                 560
Ile Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys
            565             570                 575
Gly Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys
        580             585                 590
Tyr Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg
    595             600                 605
Lys Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met
610             615                 620
Thr Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln
625             630                 635                 640
Glu Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr
            645             650                 655
Gln Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile
        660             665                 670
Phe Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly
        675             680                 685
His Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu
    690             695                 700
Asn Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys
705             710             715                 720
Ala Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val
            725             730                 735
Ile Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg
        740             745                 750
Ser Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu
    755             760                 765
Val Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys
    770             775                 780
Val Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr
785             790                 795                 800
Pro Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile
            805             810                 815
Pro Val Asp Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met
        820             825                 830
Asn Tyr Ile Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn
    835             840                 845
Pro Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp
    850             855                 860
Ser Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu
865             870                 875                 880
Leu Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala
            885             890                 895
Glu Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys
            900             905                 910
Pro Ile Tyr Phe His Thr Gln
            915
```

<210> 24
<211> 595

```
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 24
Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His
 1               5                  10                  15
Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys
            20                  25                  30
Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys
        35                  40                  45
Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
    50                  55                  60
Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
65                  70                  75                  80
Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
            85                  90                  95
Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
            100                 105                 110
Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
        115                 120                 125
Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala
    130                 135                 140
Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly
145                 150                 155                 160
Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met
            165                 170                 175
Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala
            180                 185                 190
Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe
            195                 200                 205
Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr
    210                 215                 220
Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys
225             230                 235                 240
Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg
            245                 250                 255
Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
            260                 265                 270
Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala
    275                 280                 285
Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
    290                 295                 300
Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
305                 310                 315                 320
Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
            325                 330                 335
Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
            340                 345                 350
Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
        355                 360                 365
Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
    370                 375                 380
Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Val
385                 390                 395                 400
Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
            405                 410                 415
```

```
Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
            420                 425                 430
Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
            435                 440                 445
Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
            450                 455                 460
Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
465                 470                 475                 480
Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
                485                 490                 495
Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
            500                 505                 510
His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
            515                 520                 525
Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
            530                 535                 540
Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
545                 550                 555                 560
Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
                565                 570                 575
His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
            580                 585                 590
Ala Thr Val
            595
```

```
<210> 25
<211> 6450
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 25
gagttgtgcc tggagtgatg tttaagccaa tgtcagggca aggcaacagt ccctggccgt      60
cctccagcac ctttgtaatg catatgagct cgggagacca gtacttaaag ttggaggccc     120
gggagcccag gagctggcgg agggcgttcg tcctgggagc tgcacttgct ccgtcgggtc     180
gccggcttca ccggaccgca ggctcccggg gcagggccgg ggccagagct cgcgtgtcgg     240
cgggacatgc gctgcgtcgc ctctaacctc gggctgtgct cttttttccag gtggcccgcc     300
ggtttctgag ccttctgccc tgcggggaca cggtctgcac cctgcccgcg gccacggacc     360
atgaccatga ccctccacac caaagcatct gggatggccc tactgcatca gatccaaggg     420
aacgagctgg agcccctgaa ccgtccgcag ctcaagatcc ccctggagcg gccctgggc     480
gaggtgtacc tggacagcag caagcccgcc gtgtacaact accccgaggg cgccgcctac     540
gagttcaacg ccgcggccgc cgccaacgcg caggtctacg gtcagaccgg cctcccctac     600
ggcccccggg tctgaggctg ccggcgttcggc tccaacggcc tggggggttt ccccccactc     660
aacagcgtgt ctccgagccc gctgatgcta ctgcacccgc cgccgcagct gtcgcctttc     720
ctgcagcccc acggccagca ggtgccctac tacctggaga acgagcccag cggctacacg     780
gtgcgcgagg ccggcccgcc ggcattctac aggccaaatt cagataatcg acgccagggt     840
ggcagagaaa gattggccag taccaatgac aagggaagta tggctatgga atctgccaag     900
gagactcgct actgtgcagt gtgcaatgac tatgcttcag ctaccatta tggagtctgg     960
tcctgtgagg gctgcaaggc cttcttcaag agaagtattc aaggacataa cgactatatg    1020
tgtccagcca ccaaccagtg caccattgat aaaaacagga ggaagagctg ccaggcctgc    1080
cggctccgca aatgctacga agtgggaatg atgaaaggtg ggatacgaaa agaccgaaga    1140
ggagggagaa tgttgaaaca caagcgccag agagatgatg gggagggcag gggtgaagtg    1200
gggtctgctg agacatgag agctgccaac ctttggccaa gcccgctcat gatcaaacgc    1260
tctaagaaga acagcctggc cttgtccctg acggccgacc agatggtcag tgccttgttg    1320
gatgctgagc cccccatact ctattccgag tatgatccta ccagacccctt cagtgaagct    1380
tcgatgatgg gcttactgac caacctggca gacagggagc tggttcacat gatcaactgg    1440
gcgaagaggg tgccaggctt tgtggatttg accctccatg atcaggtcca ccttctagaa    1500
tgtgcctggc tagagatcct gatgattggt ctcgtctggc gctccatgga gcacccagtg    1560
```

```
aagctactgt ttgctcctaa cttgctcttg gacaggaacc agggaaaatg tgtagagggc   1620
atggtggaga tcttcgacat gctgctggct acatcatctc ggttccgcat gatgaatctg   1680
cagggagagg agtttgtgtg cctcaaatct attattttgc ttaattctgg agtgtacaca   1740
tttctgtcca gcaccctgaa gtctctggaa gagaaggacc atatccaccg agtcctggac   1800
aagatcacag acactttgat ccacctgatg gccaaggcag gcctgaccct gcagcagcag   1860
caccagcggc tggcccagct cctcctcatc ctctcccaca tcaggcacat gagtaacaaa   1920
ggcatggagc atctgtacag catgaagtgc aagaacgtgg tgcccctcta tgacctgctg   1980
ctggagatgc tggacgccca ccgcctacat gcgcccacta gccgtggagg ggcatccgtg   2040
gaggagacgg accaaagcca cttggccact gcgggctcta cttcatcgca ttccttgcaa   2100
aagtattaca tcacggggga ggcagagggt ttccctgcca cagtctgaga gctccctggc   2160
tcccacacgg ttcagataat ccctgctgca ttttaccctc atcatgcacc actttagcca   2220
aattctgtct cctgcataca ctccggcatg catccaacac caatggcttt ctagatgagt   2280
ggccattcat ttgcttgctc agttcttagt ggcacatctt ctgtcttctg ttgggaacag   2340
ccaaagggat tccaaggcta aatctttgta acagctctct ttccccttg ctatgttact    2400
aagcgtgagg attcccgtag ctcttcacag ctgaactcag tctatggtt ggggctcaga    2460
taactctgtg catttaagct acttgtagag acccaggcct ggagagtaga cattttgcct   2520
ctgataagca cttttaaat ggctctaaga ataagccaca gcaaagaatt taaagtggct    2580
cctttaattg gtgacttgga gaaagctagg tcaagggttt attatagcac cctcttgtat   2640
tcctatggca atgcatcctt ttatgaaagt ggtacacctt aaagctttta tatgactgta   2700
gcagagtatc tggtgattgt caattcactt cccctatag gaatacaagg ggccacacag    2760
ggaaggcaga tccccctagtt ggccaagact tatttaact tgatacactg cagattcaga    2820
gtgtcctgaa gctctgcctc tggctttccg gtcatgggtt ccagttaatt catgcctccc   2880
atggacctat ggagagcaac aagttgatct tagttaagtc tccctatatg agggataagt   2940
tcctgatttt tgttttattt tttgtgttac aaaagaaagc cctccctccc tgaacttgca   3000
gtaaggtcag cttcaggacc tgttccagtg ggcactgtac ttggatcttc ccggcgtgtg   3060
tgtgccttac acaggggtga actgttcact gtggtgatgc atgatgaggg taaatggtag   3120
ttgaaaggag caggggccct ggtgttgcat ttagccctgg ggcatggagc tgaacagtac   3180
ttgtgcagga ttgttgtggc tactagagaa caagagggaa agtagggcag aaactggata   3240
cagttctgag cacagccaga cttgctcagg tggccctgca caggctgcag ctacctagga   3300
acattccttg cagaccccgc attgcctttg ggggtgccct gggatccctg gggtagtcca   3360
gctcttattc atttcccagc gtggccctgg ttggaagaag cagctgtcaa gttgtagaca   3420
gctgtgttcc tacaattggc ccagcaccct ggggcacggg agaagggtgg ggaccgttgc   3480
tgtcactact caggctgact ggggcctggt cagattacgt atgcccttgg tggtttagag   3540
ataatccaaa atcagggttt ggtttgggga agaaaatcct ccccccttcct ccccgccccc   3600
gttccctacc gcctccactc ctgccagctc atttccttca atttcctttg acctataggc   3660
taaaaaagaa aggctcattc cagccacagg gcagccttcc ctgggccttt gcttctctag   3720
cacaattatg ggttacttcc tttttcttaa caaaaagaa tgtttgattt cctctgggtg    3780
accttattgt ctgtaattga aaccctattg agaggtgatg tctgtgttag ccaatgaccc   3840
aggtagctgc tcgggcttct cttggtatgt cttgtttgga aaagtggatt tcattcattt   3900
ctgattgtcc agttaagtga tcaccaaagg actgagaatc tgggagggca aaaaaaaaaa   3960
aaaaagtttt tatgtgcact taaatttggg gacaatttta tgtatctgtg ttaaggatat   4020
gcttaagaac ataattcttt tgttgctgtt tgtttaagaa gcaccttagt ttgtttaaga   4080
agcaccttat atagtataat atatatttttt ttgaaattac attgcttgtt tatcagacaa   4140
ttgaatgtag taattctgtt ctggatttaa tttgactggg ttaacatgca aaaaccaagg   4200
aaaaatattt agttttttttt tttttttttg tatacttttc aagctacctt gtcatgtata   4260
cagtcattta tgcctaaagc ctggtgatta ttcatttaaa tgaagatcac atttcatatc   4320
aacttttgta tccacagtag acaaaatagc actaatccag atgcctattg ttggatattg   4380
aatgacagac aatcttatgt agcaaagatt atgcctgaaa aggaaaatta ttcagggcag   4440
ctaattttgc ttttaccaaa atatcagtag taatattttt ggacagtagc taatgggtca   4500
gtgggttctt tttaatgttt atacttagat tttcttttaa aaaattaaa ataaaacaaa    4560
aaaaatttct aggactagac gatgtaatac cagctaaagc caaacaatta tacagtggaa   4620
ggttttacat tattcatcca atgtgtttct attcatgtta agatactact acatttgaag   4680
tgggcagaga acatcagatg attgaaatgt tcgcccaggg gtctccagca actttggaaa   4740
tctctttgta ttttttacttg aagtgccact aatggacagc agatattttc tggctgatgt   4800
tggtattggg tgtaggaaca tgatttaaaa aaaaaactct tgcctctgct ttccccccact  4860
ctgaggcaag ttaaaatgta aagatgtga tttatctggg gggctcaggt atggtgggga    4920
agtggattca ggaatctggg gaatggcaaa tatattaaga agagtattga aagtatttgg   4980
aggaaaatgg ttaattctgg gtgtgcacca aggttcagta gagtccactt ctgccctgga   5040
gaccacaaat caactagctc catttacagc catttctaaa atggcagctt cagttctaga   5100
gaagaaagaa caacatcagc agtaaagtcc atggaatagc tagtggtctg tgtttctttt   5160
cgccattgcc tagcttgccg taatgattct ataatgccat catgcagcaa ttatgagagg   5220
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42

```
ctaggtcatc caaagagaag accctatcaa tgtaggttgc aaaatctaac ccctaaggaa          5280
gtgcagtctt tgatttgatt tccctagtaa ccttgcagat atgtttaacc aagccatagc          5340
ccatgccttt tgagggctga acaaataagg gacttactga taatttactt ttgatcacat          5400
taaggtgttc tcaccttgaa atcttataca ctgaaatggc cattgattta ggccactggc          5460
ttagagtact ccttcccctg catgacactg attacaaata cttctcctatt catacttttcc         5520
aattatgaga tggactgtgg gtactgggag tgatcactaa caccatagta atgtctaata          5580
ttcacaggca gatctgcttg gggaagctag ttatgtgaaa ggcaaataaa gtcatacagt          5640
agctcaaaag gcaaccataa ttctctttgg tgcaagtctt gggagcgtga tctagattac          5700
actgcaccat cccaagttta atcccctgaa aacttactct caactggagc aaatgaactt          5760
tggtcccaaa tatccatctt ttcagtagcg ttaattatgc tctgtttcca actgcatttc          5820
ctttccaatt gaattaaagt gtggcctcgt ttttagtcat ttaaaattgt tttctaagta          5880
attgctgcct ctattatggc acttcaattt tgcactgtct tttgagattc aagaaaaatt          5940
tctattcatt tttttgcatc caattgtgcc tgaactttta aaatatgtaa atgctgccat          6000
gttccaaacc catcgtcagt gtgtgtgttt agagctgtgc accctagaaa caacatactt          6060
gtcccatgag caggtgcctg agacacagac ccctttgcat tcacagagag gtcattggtt          6120
atagagactt gaattaataa gtgacattat gccagtttct gttctctcac aggtgataaa          6180
caatgctttt tgtgcactac atactcttca gtgtagagct cttgtttttat gggaaaaggc          6240
tcaaatgcca aattgtgttt gatggattaa tatgcccttt tgccgatgca tactattact          6300
gatgtgactc ggttttgtcg cagctttgct ttgtttaatg aaacacactt gtaaacctct          6360
tttgcacttt gaaaaagaat ccagcgggat gctcgagcac ctgtaaacaa ttttctcaac          6420
ctatttgatg ttcaaataaa gaattaaact·                                         6450
```

<210> 26

<211> 614
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 26
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Met Asn Thr Phe Gln Asp Gln Ser Gly Ser Ser Ser Asn Arg Glu Pro
1               5                   10                  15
Leu Leu Arg Cys Ser Asp Ala Arg Arg Asp Leu Glu Leu Ala Ile Gly
            20                  25                  30
Gly Val Leu Arg Ala Glu Gln Gln Ile Lys Asp Asn Leu Arg Glu Val
        35                  40                  45
Lys Ala Gln Ile His Ser Cys Ile Ser Arg His Leu Glu Cys Leu Arg
    50                  55                  60
Ser Arg Glu Val Trp Leu Tyr Glu Gln Val Asp Leu Ile Tyr Gln Leu
65                  70                  75                  80
Lys Glu Glu Thr Leu Gln Gln Gln Ala Gln Gln Leu Tyr Ser Leu Leu
                85                  90                  95
Gly Gln Phe Asn Cys Leu Thr His Gln Leu Glu Cys Thr Gln Asn Lys
            100                 105                 110
Asp Leu Ala Asn Gln Val Ser Val Cys Leu Glu Arg Leu Gly Ser Leu
        115                 120                 125
Thr Leu Lys Pro Glu Asp Ser Thr Val Leu Leu Phe Glu Ala Asp Thr
    130                 135                 140
Ile Thr Leu Arg Gln Thr Ile Thr Thr Phe Gly Ser Leu Lys Thr Ile
145                 150                 155                 160
Gln Ile Pro Glu His Leu Met Ala His Ala Ser Ser Ala Asn Ile Gly
                165                 170                 175
Pro Phe Leu Glu Lys Arg Gly Cys Ile Ser Met Pro Glu Gln Lys Ser
            180                 185                 190
Ala Ser Gly Ile Val Ala Val Pro Phe Ser Glu Trp Leu Leu Gly Ser
        195                 200                 205
```

43

```
Lys Pro Ala Ser Gly Tyr Gln Ala Pro Tyr Ile Pro Ser Thr Asp Pro
    210                 215                 220
Gln Asp Trp Leu Thr Gln Lys Gln Thr Leu Glu Asn Ser Gln Thr Ser
225                 230                 235                 240
Ser Arg Ala Cys Asn Phe Phe Asn Asn Val Gly Gly Asn Leu Lys Gly
            245                 250                 255
Leu Glu Asn Trp Leu Leu Lys Ser Glu Lys Ser Ser Tyr Gln Lys Cys
            260                 265                 270
Asn Ser His Ser Thr Thr Ser Ser Phe Ser Ile Glu Met Glu Lys Val
        275                 280                 285
Gly Asp Gln Glu Leu Pro Asp Gln Asp Glu Met Asp Leu Ser Asp Trp
    290                 295                 300
Leu Val Thr Pro Gln Glu Ser His Lys Leu Arg Lys Pro Glu Asn Gly
305                 310                 315                 320
Ser Arg Glu Thr Ser Glu Lys Phe Lys Leu Leu Phe Gln Ser Tyr Asn
            325                 330                 335
Val Asn Asp Trp Leu Val Lys Thr Asp Ser Cys Thr Asn Cys Gln Gly
            340                 345                 350
Asn Gln Pro Lys Gly Val Glu Ile Glu Asn Leu Gly Asn Leu Lys Cys
            355                 360                 365
Leu Asn Asp His Leu Glu Ala Lys Lys Pro Leu Ser Thr Pro Ser Met
        370                 375                 380
Val Thr Glu Asp Trp Leu Val Gln Asn His Gln Asp Pro Cys Lys Val
385                 390                 395                 400
Glu Glu Val Cys Arg Ala Asn Glu Pro Cys Thr Ser Phe Ala Glu Cys
            405                 410                 415
Val Cys Asp Glu Asn Cys Glu Lys Glu Ala Leu Tyr Lys Trp Leu Leu
            420                 425                 430
Lys Lys Glu Gly Lys Asp Lys Asn Gly Met Pro Val Glu Pro Lys Pro
            435                 440                 445
Glu Pro Glu Lys His Lys Asp Ser Leu Asn Met Trp Leu Cys Pro Arg
    450                 455                 460
Lys Glu Val Ile Glu Gln Thr Lys Ala Pro Lys Ala Met Thr Pro Ser
465                 470                 475                 480
Arg Ile Ala Asp Ser Phe Gln Val Ile Lys Asn Ser Pro Leu Ser Glu
            485                 490                 495
Trp Leu Ile Arg Pro Pro Tyr Lys Glu Gly Ser Pro Lys Glu Val Pro
            500                 505                 510
Gly Thr Glu Asp Arg Ala Gly Lys Gln Lys Phe Lys Ser Pro Met Asn
        515                 520                 525
Thr Ser Trp Cys Ser Phe Asn Thr Ala Asp Trp Val Leu Pro Gly Lys
        530                 535                 540
Lys Met Gly Asn Leu Ser Gln Leu Ser Ser Gly Glu Asp Lys Trp Leu
545                 550                 555                 560
Leu Arg Lys Lys Ala Gln Glu Val Leu Leu Asn Ser Pro Leu Gln Glu
            565                 570                 575
Glu His Asn Phe Pro Pro Asp His Tyr Gly Leu Pro Ala Val Cys Asp
            580                 585                 590
Leu Phe Ala Cys Met Gln Leu Lys Val Asp Lys Glu Lys Trp Leu Tyr
            595                 600                 605
Arg Thr Pro Leu Gln Met
    610
```

<210> 27
<211> 1845
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

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<400> 27
atgaatacct tccaagacca gagtggcagc tccagtaata gagaacccct tttgaggtgt    60
agtgatgcac ggagggactt ggagcttgct attggtggag ttctccgggc tgaacagcaa   120
attaaagata acttgcgaga ggtcaaagct cagattcaca gttgcataag ccgtcacctg   180
gaatgtctta gaagccgtga ggtatggctg tatgaacagg tggaccttat ttatcagctt   240
aaagaggaga cacttcaaca gcaggctcag cagctctact cgttattggg ccagttcaat   300
tgtcttactc atcaactgga gtgtacccaa aacaaagatc tagccaatca agtctctgtg   360
tgcctggaga gactgggcag tttgaccctt aagcctgaag attcaactgt cctgctcttt   420
gaagctgaca caattactct gcgccagacc atcaccacat ttgggtctct caaaaccatt   480
caaattcctg agcacttgat ggctcatgct agttcagcaa atattgggcc cttcctggag   540
aagagaggct gtatctccat gccagagcag aagtcagcat ccggtattgt agctgtccct   600
ttcagcgaat ggctccttgg aagcaaacct gccagtggtt atcaagctcc ttacataccc   660
agcaccgacc cccaggactg gcttacccaa aagcagacct ggagaacag tcagacttct   720
tccagagcct gcaatttctt caataatgtc gggggaaacc taaagggctt agaaaactgg   780
ctcctcaaga gtgaaaaatc aagttatcaa aagtgtaaca gccattccac tactagttct   840
ttctccattg aaatggaaaa ggttggagat caagagcttc ctgatcaaga tgagatggac   900
ctatcagatt ggctagtgac tccccaggaa tcccataagc tgcggaagcc tgagaatggc   960
agtcgtgaaa ccagtgagaa gtttaagctc ttattccagt cctataatgt gaatgattgg  1020
cttgtcaaga ctgactcctg taccaactgt cagggaaacc agcccaaagg tgtggagatt  1080
gaaaacctgg caatctgaa gtgcctgaat gaccacttgg aggccaagaa accattgtcc  1140
accccagca tggttacaga ggattggctt gtccagaacc atcaggaccc atgtaaggta  1200
gaggaggtgt gcagagccaa tgagccctgc acaagctttg cagagtgtgt gtgtgatgag  1260
aattgtgaga aggaggctct gtataagtgg cttctgaaga agaaggaaa ggataaaaat  1320
gggatgcctg tggaacccaa acctgagcct gagaagcata agattccct gaatatgtgg  1380
ctctgtccta gaaaagaagt aatagaacaa actaaagcac caaaggcaat gactccttct  1440
agaattgctg attccttcca gtcataaag aacagcccct tgtcggagtg gcttatcagg  1500
ccccatacа agaaggaag tcccaaggaa gtgcctggta ctgaagacag agctggcaaa  1560
cagaagttta aaagccccat gaatacttcc tggtgttcct ttaacacagc tgactgggtc  1620
ctgccaggaa agaagatggg caacctcagc cagttatctt ctggagaaga caagtggctg  1680
cttcgaaaga aggcccagga agtattactt aattcacctc tacaggagga acataacttc  1740
cccccagacc attatggcct ccctgcagtt tgtgatctct ttgcctgtat gcagcttaaa  1800
gttgataaag agaagtggtt atatcgaact cctctacaga tgtga             1845
```

```
<210> 28
<211> 474
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 28
Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu
1               5                   10                  15
Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln
                20                  25                  30
Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile
            35                  40                  45
Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu
        50                  55                  60
Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro
65                  70                  75                  80
Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys
                85                  90                  95
Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn
                100                 105                 110
Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln
            115                 120                 125
```

```
Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe
    130                 135                 140
Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln
145                 150                 155                 160
Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp
                165                 170                 175
Val Asp Gln Glu Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu
            180                 185                 190
Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln
        195                 200                 205
Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe
    210                 215                 220
Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His
225                 230                 235                 240
Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg
                245                 250                 255
Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser
                260                 265                 270
Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe
            275                 280                 285
Ala Arg Tyr Asp Arg Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala
    290                 295                 300
Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln
305                 310                 315                 320
Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe
                325                 330                 335
Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val
                340                 345                 350
Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp
            355                 360                 365
Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile
    370                 375                 380
Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn
385                 390                 395                 400
Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly
                405                 410                 415
Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile
                420                 425                 430
Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp
            435                 440                 445
Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
450                 455                 460
Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
465                 470
```

```
<210> 29
<211> 1701
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 29
ggtctctggt ctcccctctc tgagcactct gaggtcctta tgtcgtcaga agatcgagaa      60
gctcaggagg atgaattgct ggccctggca agtatttacg atggagatga atttagaaaa     120
gcagagtctg tccaaggtgg agaaaccagg atctatttgg atttgccaca gaatttcaag     180
atatttgtga gcggcaattc aaatgagtgt ctccagaata gtggctttga atacaccatt     240
tgctttctgc tccacttgt gctgaacttt gaactgccac cagattatcc atcctcttcc      300
ccaccttcat tcacacttag tggcaaatgg ctgtcaccaa ctcagctatc tgctctatgc     360
```

```
aagcacttag acaacctatg ggaagaacac cgtggcagcg tggtcctgtt tgcctggatg    420
caatttctta aggaagagac cctagcatac ttgaatattg tctctccttt tgagctcaag    480
attggttctc agaaaaaagt gcagagaagg acagctcaag cttctcccaa cacagagcta    540
gattttggag gagctgctgg atctgatgta gaccaagagg aaattgtgga tgagagagca    600
gtgcaggatg tggaatcact gtcaaatctg atccaggaaa tcttggactt tgatcaagct    660
cagcagataa aatgctttaa tagtaaattg ttcctgtgca gtatctgttt ctgtgagaag    720
ctgggtagtg aatgcatgta cttcttggag tgcaggcatg tgtactgcaa agcctgtctg    780
aaggactact ttgaaatcca gatcagagat ggccaggttc aatgcctcaa ctgcccagaa    840
ccaaagtgcc cttcggtggc cactcctggt caggtcaaag agttagtgga agcagagtta    900
tttgcccgtt atgaccgcct tctcctccag tcctccttgg acctgatggc agatgtggtg    960
tactgccccc ggccgtgctg ccagctgcct gtgatgcagg aacctggctg caccatgggt   1020
atctgctcca gctgcaattt tgccttctgt actttgtgca ggttgaccta ccatggggtc   1080
tccccatgta aggtgactgc agagaaatta atggacttac gaaatgaata cctgcaagcg   1140
gatgaggcta taaaagact tttggatcaa aggtatggta agagagtgat tcagaaggca    1200
ctggaagaga tggaaagtaa ggagtggcta gagaagaact caaagagctg cccatgttgt   1260
ggaactccca tagagaaatt agacggatgt aacaagatga catgtactgg ctgtatgcaa   1320
tatttctgtt ggatttgcat gggttctctc tctagagcaa accccttacaa acatttcaat   1380
gaccctggtt caccatgttt taaccggctg ttttatgctg tggatgttga cgacgatatt   1440
tgggaagatg aggtagaaga ctagttaact actgctcaag atatggaagt ggattgtttt   1500
tccctaatct tccgtcaagt acacaaagta actttgcggg atatttaggg tactattcat   1560
tcactcttcc tgcgtagaag atatggaaga acgaggttta tattttcatg tggtactact   1620
gaagaaggtg cattgataca tttttaaatg taagttgaga aaaatttata agccaaaggt   1680
tcagaaaatt aaactacaga a                                              1701
```

<210> 30
<211> 444
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 30
```
Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
 1               5                  10                  15
Pro Pro Pro Ser Tyr Gly His Gln Pro Gln Thr Gly Ser Gly Glu Ser
                20                  25                  30
Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
            35                  40                  45
Pro Arg Ser Pro Lys Pro Ala Ala Pro Ala Ala Pro Pro Phe Ser Ser
        50                  55                  60
Ser Ser Gly Val Leu Gly Thr Gly Leu Cys Glu Leu Asp Arg Leu Leu
65                  70                  75                  80
Gln Glu Leu Asn Ala Thr Gln Phe Asn Ile Thr Asp Glu Ile Met Ser
                85                  90                  95
Gln Phe Pro Ser Ser Lys Val Ala Ser Gly Glu Gln Lys Glu Asp Gln
            100                 105                 110
Ser Glu Asp Lys Lys Arg Pro Ser Leu Pro Ser Ser Pro Ser Pro Gly
        115                 120                 125
Leu Pro Lys Ala Ser Ala Thr Ser Ala Thr Leu Glu Leu Asp Arg Leu
    130                 135                 140
Met Ala Ser Leu Pro Asp Phe Arg Val Gln Asn His Leu Pro Ala Ser
145                 150                 155                 160
Gly Pro Thr Gln Pro Pro Val Val Ser Ser Thr Asn Glu Gly Ser Pro
                165                 170                 175
Ser Pro Pro Glu Pro Thr Ala Lys Gly Ser Leu Asp Thr Met Leu Gly
            180                 185                 190
Leu Leu Gln Ser Asp Leu Ser Arg Arg Gly Val Pro Thr Gln Ala Lys
        195                 200                 205
```

                                    47

```
Gly Leu Cys Gly Ser Cys Asn Lys Pro Ile Ala Gly Gln Val Val Thr
    210                 215                 220
Ala Leu Gly Arg Ala Trp His Pro Glu His Phe Val Cys Gly Gly Cys
225                 230                 235                 240
Ser Thr Ala Leu Gly Gly Ser Ser Phe Phe Glu Lys Asp Gly Ala Pro
            245                 250                 255
Phe Cys Pro Glu Cys Tyr Phe Glu Arg Phe Ser Pro Arg Cys Gly Phe
            260                 265                 270
Cys Asn Gln Pro Ile Arg His Lys Met Val Thr Ala Leu Gly Thr His
            275                 280                 285
Trp His Pro Glu His Phe Cys Cys Val Ser Cys Gly Glu Pro Phe Gly
    290                 295                 300
Asp Glu Gly Phe His Glu Arg Glu Gly Arg Pro Tyr Cys Arg Arg Asp
305                 310                 315                 320
Phe Leu Gln Leu Phe Ala Pro Arg Cys Gln Gly Cys Gln Gly Pro Ile
            325                 330                 335
Leu Asp Asn Tyr Ile Ser Ala Leu Ser Leu Leu Trp His Pro Asp Cys
            340                 345                 350
Phe Val Cys Arg Glu Cys Phe Ala Pro Phe Ser Gly Gly Ser Phe Phe
            355                 360                 365
Glu His Glu Gly Arg Pro Leu Cys Glu Asn His Phe His Ala Arg Arg
    370                 375                 380
Gly Ser Leu Trp Pro Thr Cys Gly Leu Pro Val Thr Gly Arg Cys Val
385                 390                 395                 400
Ser Ala Leu Gly Arg Arg Phe His Pro Asp His Phe Ala Cys Thr Phe
            405                 410                 415
Cys Leu Arg Pro Leu Thr Lys Gly Ser Phe Gln Glu Arg Ala Gly Lys
            420                 425                 430
Pro Tyr Cys Gln Pro Cys Phe Leu Lys Leu Phe Gly
            435                 440
```

```
<210> 31
<211> 1335
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 31
atgccaaggt cagggggctcc caaagagcgc cctgcggagc ctctcacccc tcccccatcc      60
tatggccacc agccacagac agggtctggg gagtcttcag gagcctcggg ggacaaggac     120
cacctgtaca gcacggtatg caagcctcgg tccccaaagc ctgcagcccc ggccgcccct     180
ccattctcct cttccagcgg tgtcttgggt accgggctct gtgagctaga tcggttgctt     240
caggaactta atgccactca gttcaacatc acagatgaaa tcatgtctca gttcccatct     300
agcaaggtgg cttcaggaga gcagaaggag gaccagtctg aagataagaa aagacccagc     360
ctcccttcca gcccgtctcc tggcctccca aaggcttctg ccacctcagc cactctggag     420
ctggatagac tgatggcctc actccctgac ttccgcgttc aaaaccatct tccagcctct     480
gggccaactc agccaccggt ggtgagctcc acaaatgagg ctcccatc cccaccagag       540
ccgactgcaa agggcagcct agacaccatg ctggggctgc tgcagtccga cctcagccgc     600
cggggtgttc ccacccaggc caaaggcctc tgtggctcct gcaataaacc tattgctggg     660
caagtggtga cggctctggg ccgcgcctgg caccccgagc acttcgtttg cggaggctgt     720
tccaccgccc tgggaggcag cagcttcttc gagaaggatg gagcccccctt ctgccccgag     780
tgctactttg agcgcttctc gccaagatgt ggcttctgca accagcccat ccgacacaag     840
atggtgaccg ccttgggcac tcactggcac ccagagcatt tctgctgcgt cagttgcggg     900
gagcccttcg gagatgaggg tttccacgag cgcgaggggcc gccctactg ccgccgggac       960
ttcctgcagc tgttcgcccc cgctgccag ggctgccagg gccccatcct ggataactac     1020
atctcggcgc tcagcctgct ctggcaccccg gactgtttcg tctgcaggga atgcttcgcg     1080
cccttctcgg gaggcagctt tttcgagcac gagggccgcc cgttgtgcga gaaccacttc     1140
cacgcacgac gcggctcgct gtggcccacg tgtggcctcc ctgtgaccgg ccgctgcgtg     1200
```

```
tcggccctgg gtcgccgctt ccacccggac cacttcgcat gcaccttctg cctgcgcccg    1260
ctcaccaagg ggtccttcca ggagcgcgcc ggcaagccct actgccagcc ctgcttcctg    1320
aagctcttcg gctga                                                     1335
```

```
<210> 32
<211> 216
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 32
Met Ala Ala Gln Gly Glu Pro Gln Val Gln Phe Lys Leu Val Leu Val
1               5                   10                  15
Gly Asp Gly Gly Thr Gly Lys Thr Thr Phe Val Lys Arg His Leu Thr
            20                  25                  30
Gly Glu Phe Glu Lys Lys Tyr Val Ala Thr Leu Gly Val Glu Val His
        35                  40                  45
Pro Leu Val Phe His Thr Asn Arg Gly Pro Ile Lys Phe Asn Val Trp
    50                  55                  60
Asp Thr Ala Gly Gln Glu Lys Phe Gly Gly Leu Arg Asp Gly Tyr Tyr
65                  70                  75                  80
Ile Gln Ala Gln Cys Ala Ile Ile Met Phe Asp Val Thr Ser Arg Val
                85                  90                  95
Thr Tyr Lys Asn Val Pro Asn Trp His Arg Asp Leu Val Arg Val Cys
            100                 105                 110
Glu Asn Ile Pro Ile Val Leu Cys Gly Asn Lys Val Asp Ile Lys Asp
        115                 120                 125
Arg Lys Val Lys Ala Lys Ser Ile Val Phe His Arg Lys Lys Asn Leu
    130                 135                 140
Gln Tyr Tyr Asp Ile Ser Ala Lys Ser Asn Tyr Asn Phe Glu Lys Pro
145                 150                 155                 160
Phe Leu Trp Leu Ala Arg Lys Leu Ile Gly Asp Pro Asn Leu Glu Phe
                165                 170                 175
Val Ala Met Pro Ala Leu Ala Pro Pro Glu Val Val Met Asp Pro Ala
            180                 185                 190
Leu Ala Ala Gln Tyr Glu His Asp Leu Glu Val Ala Gln Thr Thr Ala
        195                 200                 205
Leu Pro Asp Glu Asp Asp Asp Leu
    210                 215
```

```
<210> 33
<211> 1566
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 33
ggcgcttctg gaaggaacgc cgcgatggct gcgcagggag agccccaggt ccagttcaaa     60
cttgtattgg ttggtgatgg tggtactgga aaaacgacct tcgtgaaacg tcatttgact    120
ggtgaatttg agaagaagta tgtagccacc ttgggtgttg aggttcatcc cctagtgttc    180
cacaccaaca gaggacctat taagttcaat gtatgggaca cagccggcca ggagaaattc    240
ggtggactga gagatggcta ttatatccaa gcccagtgtg ccatcataat gtttgatgta    300
acatcgagag ttacttacaa gaatgtgcct aactggcata gagatctggt acgagtgtgt    360
gaaaacatcc ccattgtgtt gtgtggcaac aaagtggata ttaaggacag gaaagtgaag    420
gcgaaatcca ttgtcttcca ccgaaagaag aatcttcagt actacgacat ttctgccaaa    480
```

```
agtaactaca actttgaaaa gcccttcctc tggcttgcta ggaagctcat tggagaccct    540
aacttggaat ttgttgccat gcctgctctc gccccaccag aagttgtcat ggacccagct    600
ttggcagcac agtatgagca cgacttagag gttgctcaga caactgctct cccggatgag    660
gatgatgacc tgtgagaatg aagctggagc ccagcgtcag aagtctagtt ttataggcag    720
ctgtcctgtg atgtcagcgg tgcagcgtgt gtgccacctc attattatct agctaagcgg    780
aacatgtgct ttatctgtgg gatgctgaag gagatgagtg ggcttcggag tgaatgtggc    840
agtttaaaaa ataacttcat tgtttggacc tgcatattta gctgtttgga cgcagttgat    900
tccttgagtt tcatatataa gactgctgca gtcacatcac aatattcagt ggtgaaatct    960
tgtttgttac tgtcattccc attccttttc tttagaatca gaataaagtt gtatttcaaa   1020
tatctaagca agtgaactca tcccttgttt ataaatagca tttggaaacc actaaagtag   1080
ggaagtttta tgccatgtta atatttgaat tgccttgctt ttatcactta atttgaaatc   1140
tattgggtta atttctccct atgtttattt ttgtacattt gagccatgtc acacaaactg   1200
atgatgacag gtcagcagta ttctatttgg ttagaagggt tacatggtgt aaatattagt   1260
gcagttaagc taaagcagtg tttgctccac cttcatattg ctaggtagg tcacctagg    1320
gaagcacttg ctcaaaatct gtgacctgtc agaataaaaa tgtggtttgt acatatcaaa   1380
tagatatttt aagggtaata ttttctttta tggcaaaagt aatcatgttt taatgtagaa   1440
cctcaaacag gatggaacat cagtggatgg caggaggttg ggaattcttg ctgttaaaaa   1500
taattacaaa ttttgcactt tttgtttgaa tgttagatgc ttagtgtgaa gttgatacgc   1560
aagccg                                                               1566
```

<210> 34
<211> 2427
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 34
```
Met Pro Leu Lys Thr Arg Thr Ala Leu Ser Asp Asp Pro Asp Ser Ser
1               5                   10                  15
Thr Ser Thr Leu Gly Asn Met Leu Glu Leu Pro Gly Thr Ser Ser Ser
            20                  25                  30
Ser Thr Ser Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr
        35                  40                  45
Pro Leu Lys Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg
    50                  55                  60
Arg Pro Trp Trp Pro Cys Arg Ile Cys Ser Asp Pro Leu Ile Asn Thr
65                  70                  75                  80
His Ser Lys Met Lys Val Ser Asn Arg Arg Pro Tyr Arg Gln Tyr Tyr
                85                  90                  95
Val Glu Ala Phe Gly Asp Pro Ser Glu Arg Ala Trp Val Ala Gly Lys
            100                 105                 110
Ala Ile Val Met Phe Glu Gly Arg His Gln Phe Glu Glu Leu Pro Val
        115                 120                 125
Leu Arg Arg Arg Gly Lys Gln Lys Glu Lys Gly Tyr Arg His Lys Val
    130                 135                 140
Pro Gln Lys Ile Leu Ser Lys Trp Glu Ala Ser Val Gly Leu Ala Glu
145                 150                 155                 160
Gln Tyr Asp Val Pro Lys Gly Ser Lys Asn Arg Lys Cys Ile Pro Gly
                165                 170                 175
Ser Ile Lys Leu Asp Ser Glu Glu Asp Met Pro Phe Glu Asp Cys Thr
            180                 185                 190
Asn Asp Pro Glu Ser Glu His Asp Leu Leu Leu Asn Gly Cys Leu Lys
        195                 200                 205
Ser Leu Ala Phe Asp Ser Glu His Ser Ala Asp Glu Lys Glu Lys Pro
    210                 215                 220
Cys Ala Lys Ser Arg Ala Arg Lys Ser Ser Asp Asn Pro Lys Arg Thr
225                 230                 235                 240
```

Ser Val Lys Lys Gly His Ile Gln Phe Glu Ala His Lys Asp Glu Arg
            245   250   255

Arg Gly Lys Ile Pro Glu Asn Leu Gly Leu Asn Phe Ile Ser Gly Asp
            260   265   270

Ile Ser Asp Thr Gln Ala Ser Asn Glu Leu Ser Arg Ile Ala Asn Ser
            275   280   285

Leu Thr Gly Ser Asn Thr Ala Pro Gly Ser Phe Leu Phe Ser Ser Cys
    290   295   300

Gly Lys Asn Thr Ala Lys Lys Glu Phe Glu Thr Ser Asn Gly Asp Ser
305   310   315   320

Leu Leu Gly Leu Pro Glu Gly Ala Leu Ile Ser Lys Cys Ser Arg Glu
            325   330   335

Lys Asn Lys Pro Gln Arg Ser Leu Val Cys Gly Ser Lys Val Lys Leu
            340   345   350

Cys Tyr Ile Gly Ala Gly Asp Glu Glu Lys Arg Ser Asp Ser Ile Ser
            355   360   365

Ile Cys Thr Thr Ser Asp Asp Gly Ser Ser Asp Leu Asp Pro Ile Glu
    370   375   380

His Ser Ser Glu Ser Asp Asn Ser Val Leu Glu Ile Pro Asp Ala Phe
385   390   395   400

Asp Arg Thr Glu Asn Met Leu Ser Met Gln Lys Asn Glu Lys Ile Lys
            405   410   415

Tyr Ser Arg Phe Ala Ala Thr Asn Thr Arg Val Lys Ala Lys Gln Lys
            420   425   430

Pro Leu Ile Ser Asn Ser His Thr Asp His Leu Met Gly Cys Thr Lys
            435   440   445

Ser Ala Glu Pro Gly Thr Glu Thr Ser Gln Val Asn Leu Ser Asp Leu
    450   455   460

Lys Ala Ser Thr Leu Val His Lys Pro Gln Ser Asp Phe Thr Asn Asp
465   470   475   480

Ala Leu Ser Pro Lys Phe Asn Leu Ser Ser Ser Ile Ser Ser Glu Asn
            485   490   495

Ser Leu Ile Lys Gly Gly Ala Ala Asn Gln Ala Leu Leu His Ser Lys
            500   505   510

Ser Lys Gln Pro Lys Phe Arg Ser Ile Lys Cys Lys His Lys Glu Asn
            515   520   525

Pro Val Met Ala Glu Pro Pro Val Ile Asn Glu Glu Cys Ser Leu Lys
    530   535   540

Cys Cys Ser Ser Asp Thr Lys Gly Ser Pro Leu Ala Ser Ile Ser Lys
545   550   555   560

Ser Gly Lys Val Asp Gly Leu Lys Leu Leu Asn Asn Met His Glu Lys
            565   570   575

Thr Arg Asp Ser Ser Asp Ile Glu Thr Ala Val Val Lys His Val Leu
            580   585   590

Ser Glu Leu Lys Glu Leu Ser Tyr Arg Ser Leu Gly Glu Asp Val Ser
            595   600   605

Asp Ser Gly Thr Ser Lys Pro Ser Lys Pro Leu Leu Phe Ser Ser Ala
    610   615   620

Ser Ser Gln Asn His Ile Pro Ile Glu Pro Asp Tyr Lys Phe Ser Thr
625   630   635   640

Leu Leu Met Met Leu Lys Asp Met His Asp Ser Lys Thr Lys Glu Gln
            645   650   655

Arg Leu Met Thr Ala Gln Asn Leu Val Ser Tyr Arg Ser Pro Gly Arg
            660   665   670

Gly Asp Cys Ser Thr Asn Ser Pro Val Gly Val Ser Lys Val Leu Val
            675   680   685

Ser Gly Gly Ser Thr His Asn Ser Glu Lys Lys Gly Asp Gly Thr Gln
    690   695   700

Asn Ser Ala Asn Pro Ser Pro Ser Gly Gly Asp Ser Ala Leu Ser Gly
705   710   715   720

```
Glu Leu Ser Ala Ser Leu Pro Gly Leu Leu Ser Asp Lys Arg Asp Leu
        725                 730                 735
Pro Ala Ser Gly Lys Ser Arg Ser Asp Cys Val Thr Arg Arg Asn Cys
        740                 745                 750
Gly Arg Ser Lys Pro Ser Ser Lys Leu Arg Asp Ala Phe Ser Ala Gln
        755                 760                 765
Met Val Lys Asn Thr Val Asn Arg Lys Ala Leu Lys Thr Glu Arg Lys
    770                 775                 780
Arg Lys Leu Asn Gln Leu Pro Ser Val Thr Leu Asp Ala Val Leu Gln
785                 790                 795                 800
Gly Asp Arg Glu Arg Gly Gly Ser Leu Arg Gly Gly Ala Glu Asp Pro
                805                 810                 815
Ser Lys Glu Asp Pro Leu Gln Ile Met Gly His Leu Thr Ser Glu Asp
            820                 825                 830
Gly Asp His Phe Ser Asp Val His Phe Asp Ser Lys Val Lys Gln Ser
        835                 840                 845
Asp Pro Gly Lys Ile Ser Glu Lys Gly Leu Ser Phe Glu Asn Gly Lys
    850                 855                 860
Gly Pro Glu Leu Asp Ser Val Met Asn Ser Glu Asn Asp Glu Leu Asn
865                 870                 875                 880
Gly Val Asn Gln Val Val Pro Lys Lys Arg Trp Gln Arg Leu Asn Gln
                885                 890                 895
Arg Arg Thr Lys Pro Arg Lys Arg Met Asn Arg Phe Lys Glu Lys Glu
            900                 905                 910
Asn Ser Glu Cys Ala Phe Arg Val Leu Leu Pro Ser Asp Pro Val Gln
        915                 920                 925
Glu Gly Arg Asp Glu Phe Pro Glu His Arg Thr Pro Ser Ala Ser Ile
    930                 935                 940
Leu Glu Glu Pro Leu Thr Glu Gln Asn His Ala Asp Cys Leu Asp Ser
945                 950                 955                 960
Ala Gly Pro Arg Leu Asn Val Cys Asp Lys Ser Ser Ala Ser Ile Gly
                965                 970                 975
Asp Met Glu Lys Glu Pro Gly Ile Pro Ser Leu Thr Pro Gln Ala Glu
            980                 985                 990
Leu Pro Glu Pro Ala Val Arg Ser Glu Lys Lys Arg Leu Arg Lys Pro
        995                 1000                1005
Ser Lys Trp Leu Leu Glu Tyr Thr Glu Glu Tyr Asp Gln Ile Phe Ala
    1010                1015                1020
Pro Lys Lys Lys Gln Lys Lys Val Gln Glu Gln Val His Lys Val Ser
1025                1030                1035                1040
Ser Arg Cys Glu Glu Glu Ser Leu Leu Ala Arg Gly Arg Ser Ser Ala
                1045                1050                1055
Gln Asn Lys Gln Val Asp Glu Asn Ser Leu Ile Ser Thr Lys Glu Glu
            1060                1065                1070
Pro Pro Val Leu Glu Arg Glu Ala Pro Phe Leu Glu Gly Pro Leu Ala
        1075                1080                1085
Gln Ser Glu Leu Gly Gly Gly His Ala Glu Leu Pro Gln Leu Thr Leu
    1090                1095                1100
Ser Val Pro Val Ala Pro Glu Val Ser Pro Arg Pro Ala Leu Glu Ser
1105                1110                1115                1120
Glu Glu Leu Leu Val Lys Thr Pro Gly Asn Tyr Glu Ser Lys Arg Gln
                1125                1130                1135
Arg Lys Pro Thr Lys Lys Leu Leu Glu Ser Asn Asp Leu Asp Pro Gly
            1140                1145                1150
Phe Met Pro Lys Lys Gly Asp Leu Gly Leu Ser Lys Lys Cys Tyr Glu
        1155                1160                1165
Ala Gly His Leu Glu Asn Gly Ile Thr Glu Ser Cys Ala Thr Ser Tyr
    1170                1175                1180
Ser Lys Asp Phe Gly Gly Gly Thr Thr Lys Ile Phe Asp Lys Pro Arg
1185                1190                1195                1200
```

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Lys Arg Lys Arg Gln Arg His Ala Ala Ala Lys Met Gln Cys Lys Lys
            1205              1210              1215
Val Lys Asn Asp Asp Ser Ser Lys Glu Ile Pro Gly Ser Glu Gly Glu
            1220              1225              1230
Leu Met Pro His Arg Thr Ala Thr Ser Pro Lys Glu Thr Val Glu Glu
            1235              1240              1245
Gly Val Glu His Asp Pro Gly Met Pro Ala Ser Lys Lys Met Gln Gly
          1250              1255              1260
Glu Arg Gly Gly Gly Ala Ala Leu Lys Glu Asn Val Cys Gln Asn Cys
1265              1270              1275              1280
Glu Lys Leu Gly Glu Leu Leu Leu Cys Glu Ala Gln Cys Cys Gly Ala
            1285              1290              1295
Phe His Leu Glu Cys Leu Gly Leu Thr Glu Met Pro Arg Gly Lys Phe
            1300              1305              1310
Ile Cys Asn Glu Cys Arg Thr Gly Ile His Thr Cys Phe Val Cys Lys
            1315              1320              1325
Gln Ser Gly Glu Asp Val Lys Arg Cys Leu Leu Pro Leu Cys Gly Lys
            1330              1335              1340
Phe Tyr His Glu Glu Cys Val Gln Lys Tyr Pro Pro Thr Val Met Gln
1345              1350              1355              1360
Asn Lys Gly Phe Arg Cys Ser Leu His Ile Cys Ile Thr Cys His Ala
            1365              1370              1375
Ala Asn Pro Ala Asn Val Ser Ala Ser Lys Gly Arg Leu Met Arg Cys
            1380              1385              1390
Val Arg Cys Pro Val Ala Tyr His Ala Asn Asp Phe Cys Leu Ala Ala
            1395              1400              1405
Gly Ser Lys Ile Leu Ala Ser Asn Ser Ile Ile Cys Pro Asn His Phe
          1410              1415              1420
Thr Pro Arg Arg Gly Cys Arg Asn His Glu His Val Asn Val Ser Trp
1425              1430              1435              1440
Cys Phe Val Cys Ser Glu Gly Gly Ser Leu Leu Cys Cys Asp Ser Cys
            1445              1450              1455
Pro Ala Ala Phe His Arg Glu Cys Leu Asn Ile Asp Ile Pro Glu Gly
            1460              1465              1470
Asn Trp Tyr Cys Asn Asp Cys Lys Ala Gly Lys Lys Pro His Tyr Arg
            1475              1480              1485
Glu Ile Val Trp Val Lys Val Gly Arg Tyr Arg Trp Trp Pro Ala Glu
          1490              1495              1500
Ile Cys His Pro Arg Ala Val Pro Ser Asn Ile Asp Lys Met Arg His
1505              1510              1515              1520
Asp Val Gly Glu Phe Pro Val Leu Phe Phe Gly Ser Asn Asp Tyr Leu
            1525              1530              1535
Trp Thr His Gln Ala Arg Val Phe Pro Tyr Met Glu Gly Asp Val Ser
            1540              1545              1550
Ser Lys Asp Lys Met Gly Lys Gly Val Asp Gly Thr Tyr Lys Lys Ala
            1555              1560              1565
Leu Gln Glu Ala Ala Ala Arg Phe Glu Glu Leu Lys Ala Gln Lys Glu
            1570              1575              1580
Leu Arg Gln Leu Gln Glu Asp Arg Lys Asn Asp Lys Lys Pro Pro Pro
1585              1590              1595              1600
Tyr Lys His Ile Lys Val Asn Arg Pro Ile Gly Arg Val Gln Ile Phe
            1605              1610              1615
Thr Ala Asp Leu Ser Glu Ile Pro Arg Cys Asn Cys Lys Ala Thr Asp
            1620              1625              1630
Glu Asn Pro Cys Gly Ile Asp Ser Glu Cys Ile Asn Arg Met Leu Leu
            1635              1640              1645
Tyr Glu Cys His Pro Thr Val Cys Pro Ala Gly Gly Arg Cys Gln Asn
            1650              1655              1660
Gln Cys Phe Ser Lys Arg Gln Tyr Pro Glu Val Glu Ile Phe Arg Thr
1665              1670              1675              1680
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Leu Gln Arg Gly Trp Gly Leu Arg Thr Lys Thr Asp Ile Lys Lys Gly
          1685   1690   1695
Glu Phe Val Asn Glu Tyr Val Gly Glu Leu Ile Asp Glu Glu Glu Cys
          1700   1705   1710
Arg Ala Arg Ile Arg Tyr Ala Gln Glu His Asp Ile Thr Asn Phe Tyr
          1715   1720   1725
Met Leu Thr Leu Asp Lys Asp Arg Ile Ile Asp Ala Gly Pro Lys Gly
          1730   1735   1740
Asn Tyr Ala Arg Phe Met Asn His Cys Cys Gln Pro Asn Cys Glu Thr
1745   1750   1755   1760
Gln Lys Trp Ser Val Asn Gly Asp Thr Arg Val Gly Leu Phe Ala Leu
          1765   1770   1775
Ser Asp Ile Lys Ala Gly Thr Glu Leu Thr Phe Asn Tyr Asn Leu Glu
          1780   1785   1790
Cys Leu Gly Asn Gly Lys Thr Val Cys Lys Cys Gly Ala Pro Asn Cys
          1795   1800   1805
Ser Gly Phe Leu Gly Val Arg Pro Lys Asn Gln Pro Ile Ala Thr Glu
          1810   1815   1820
Glu Lys Ser Lys Lys Phe Lys Lys Lys Gln Gln Gly Lys Arg Arg Thr
1825   1830   1835   1840
Gln Gly Glu Ile Thr Lys Glu Arg Glu Asp Glu Cys Phe Ser Cys Gly
          1845   1850   1855
Asp Ala Gly Gln Leu Val Ser Cys Lys Lys Pro Gly Cys Pro Lys Val
          1860   1865   1870
Tyr His Ala Asp Cys Leu Asn Leu Thr Lys Arg Pro Ala Gly Lys Trp
          1875   1880   1885
Glu Cys Pro Trp His Gln Cys Asp Ile Cys Gly Lys Glu Ala Ala Ser
          1890   1895   1900
Phe Cys Glu Met Cys Pro Ser Ser Phe Cys Lys Gln His Arg Glu Gly
1905   1910   1915   1920
Met Leu Phe Ile Ser Lys Leu Asp Gly Arg Leu Ser Cys Thr Glu His
          1925   1930   1935
Asp Pro Cys Gly Pro Asn Pro Leu Glu Pro Gly Glu Ile Arg Glu Tyr
          1940   1945   1950
Val Pro Pro Pro Val Pro Leu Pro Pro Gly Pro Ser Thr His Leu Ala
          1955   1960   1965
Glu Gln Ser Thr Gly Met Ala Ala Gln Ala Pro Lys Met Ser Asp Lys
          1970   1975   1980
Pro Pro Ala Asp Thr Asn Gln Met Leu Ser Leu Ser Lys Lys Ala Leu
1985   1990   1995   2000
Ala Gly Thr Cys Gln Arg Pro Leu Leu Pro Glu Arg Pro Leu Glu Arg
          2005   2010   2015
Thr Asp Ser Arg Pro Gln Pro Leu Asp Lys Val Arg Asp Leu Ala Gly
          2020   2025   2030
Ser Gly Thr Lys Ser Gln Ser Leu Val Ser Ser Gln Arg Pro Leu Asp
          2035   2040   2045
Arg Pro Pro Ala Val Ala Gly Pro Arg Pro Gln Leu Ser Asp Lys Pro
          2050   2055   2060
Ser Pro Val Thr Ser Pro Ser Ser Ser Pro Ser Val Arg Ser Gln Pro
2065   2070   2075   2080
Leu Glu Arg Pro Leu Gly Thr Ala Asp Pro Arg Leu Asp Lys Ser Ile
          2085   2090   2095
Gly Ala Ala Ser Pro Arg Pro Gln Ser Leu Glu Lys Thr Ser Val Pro
          2100   2105   2110
Thr Gly Leu Arg Leu Pro Pro Pro Asp Arg Leu Leu Ile Thr Ser Ser
          2115   2120   2125
Pro Lys Pro Gln Thr Ser Asp Arg Pro Thr Asp Lys Pro His Ala Ser
          2130   2135   2140
Leu Ser Gln Arg Leu Pro Pro Pro Glu Lys Val Leu Ser Ala Val Val
2145   2150   2155   2160

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Gln Thr Leu Val Ala Lys Glu Lys Ala Leu Arg Pro Val Asp Gln Asn
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Thr Gln Ser Lys Asn Arg Ala Ala Leu Val Met Asp Leu Ile Asp Leu
              2180                  2185                  2190
Thr Pro Arg Gln Lys Glu Arg Ala Ala Ser Pro His Gln Val Thr Pro
          2195                  2200                  2205
Gln Ala Asp Glu Lys Met Pro Val Leu Glu Ser Ser Ser Trp Pro Ala
          2210                  2215                  2220
Ser Lys Gly Leu Gly His Met Pro Arg Ala Val Glu Lys Gly Cys Val
2225                  2230                  2235                  2240
Ser Asp Pro Leu Gln Thr Ser Gly Lys Ala Ala Ala Pro Ser Glu Asp
              2245                  2250                  2255
Pro Trp Gln Ala Val Lys Ser Leu Thr Gln Ala Arg Leu Leu Ser Gln
              2260                  2265                  2270
Pro Pro Ala Lys Ala Phe Leu Tyr Glu Pro Thr Thr Gln Ala Ser Gly
          2275                  2280                  2285
Arg Ala Ser Ala Gly Ala Glu Gln Thr Pro Gly Pro Leu Ser Gln Ser
          2290                  2295                  2300
Pro Gly Leu Val Lys Gln Ala Lys Gln Met Val Gly Gly Gln Gln Leu
2305                  2310                  2315                  2320
Pro Ala Leu Ala Ala Lys Ser Gly Gln Ser Phe Arg Ser Leu Gly Lys
              2325                  2330                  2335
Ala Pro Ala Ser Leu Pro Thr Glu Glu Lys Lys Leu Val Thr Thr Glu
              2340                  2345                  2350
Gln Ser Pro Trp Ala Leu Gly Lys Ala Ser Ser Arg Ala Gly Leu Trp
          2355                  2360                  2365
Pro Ile Val Ala Gly Gln Thr Leu Ala Gln Ser Cys Trp Ser Ala Gly
          2370                  2375                  2380
Ser Thr Gln Thr Leu Ala Gln Thr Cys Trp Ser Leu Gly Arg Gly Gln
2385                  2390                  2395                  2400
Asp Pro Lys Pro Glu Gln Asn Thr Leu Pro Ala Leu Asn Gln Ala Pro
              2405                  2410                  2415
Ser Ser His Lys Cys Ala Glu Ser Glu Gln Lys
              2420                  2425
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<210> 35
<211> 7707
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 35

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cagcccttc ggatgatcca gattccagta ccagtacatt aggaaacatg ctagaattac    180
ctggaacttc atcatcatct acttcacagg aattgccatt ttgtcaacct aagaaaaagt    240
ctacgccact gaagtatgaa gttggagatc tcatctgggc aaaattcaag agacgcccat    300
ggtggccctg caggatttgt tctgatccgt tgattaacac acattcaaaa atgaaagttt    360
ccaaccggag ccctatcgg cagtactacg tggaggcttt tggagatcct tctgagagag    420
cctgggtggc tggaaaagca atcgtcatgt ttgaaggcag acatcaattc gaagagctac    480
ctgtccttag gagaagaggg aaacagaaag aaaaaggata taggcataag gttcctcaga    540
aaattttgag taaatgggaa gccagtgttg gacttgcaga acagtatgat gttcccaagg    600
ggtcaaagaa ccgaaaatgt attcctggtt caatcaagtt ggacagtgaa gaagatatgc    660
catttgaaga ctgcacaaat gatcctgagt cagaacatga cctgttgctt aatggctgtt    720
tgaaatcact ggcttttgat tctgaacatt ctgcagatga gaaggaaaag ccttgtgcta    780
aatctcgagc cagaaagagc tctgataatc caaaaggac tagtgtgaaa aagggccaca    840
tacaatttga agcacataaa gatgaacgga ggggaaagat tccagagaac cttggcctaa    900
actttatctc tggggatata tctgatacgc aggcctctaa tgaactttcc aggatagcaa    960
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atagcctcac aggggtccaac actgccccag gaagttttct gttttcttcc tgtggaaaaa   1020
acactgcaaa gaaagaattt gagacttcaa atggtgactc tttattgggc ttgcctgagg   1080
gtgctttgat ctcaaagtgt tctcgagaga agaataaacc ccaacgaagc ctggtgtgtg   1140
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<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 36

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Gly Asn Gly Gln Ser Asn Phe Ser Glu Pro Leu Asn Gly Cys Thr Met
        35                  40                  45
Gln Leu Ser Thr Val Ser Gly Thr Ser Gln Asn Ala Tyr Gly Gln Asp
    50                  55                  60
Ser Pro Ser Cys Tyr Ile Pro Leu Arg Arg Leu Gln Asp Leu Ala Ser
65              70                  75                  80
Met Ile Asn Val Glu Tyr Leu Asn Gly Ser Ala Asp Gly Ser Glu Ser
                85                  90                  95
Phe Gln Asp Pro Glu Lys Ser Asp Ser Arg Ala Gln Thr Pro Ile Val
            100                 105                 110
Cys Thr Ser Leu Ser Pro Gly Gly Pro Thr Ala Leu Ala Met Lys Gln
        115                 120                 125
Glu Pro Ser Cys Asn Asn Ser Pro Glu Leu Gln Val Lys Val Thr Lys
    130                 135                 140
Thr Ile Lys Asn Gly Phe Leu His Phe Glu Asn Phe Thr Cys Val Asp
145             150                 155                 160
Asp Ala Asp Val Asp Ser Glu Met Asp Pro Glu Gln Pro Val Thr Glu
                165                 170                 175
Asp Glu Ser Ile Glu Glu Ile Phe Glu Glu Thr Gln Thr Asn Ala Thr
            180                 185                 190
Cys Asn Tyr Glu Thr Lys Ser Glu Asn Gly Val Lys Val Ala Met Gly
        195                 200                 205
Ser Glu Gln Asp Ser Thr Pro Glu Ser Arg His Gly Ala Val Lys Ser
    210                 215                 220
Pro Phe Leu Pro Leu Ala Pro Gln Thr Glu Thr Gln Lys Asn Lys Gln
225             230                 235                 240
Arg Asn Glu Val Asp Gly Ser Asn Glu Lys Ala Ala Leu Leu Pro Ala
            245                 250                 255
Pro Phe Ser Leu Gly Asp Thr Asn Ile Thr Ile Glu Glu Gln Leu Asn
            260                 265                 270
Ser Ile Asn Leu Ser Phe Gln Asp Asp Pro Asp Ser Ser Thr Ser Thr
    275                 280                 285
Leu Gly Asn Met Leu Glu Leu Pro Gly Thr Ser Ser Ser Ser Thr Ser
    290                 295                 300
Gln Glu Leu Pro Phe Cys Gln Pro Lys Lys Lys Ser Thr Pro Leu Lys
305             310                 315                 320
Tyr Glu Val Gly Asp Leu Ile Trp Ala Lys Phe Lys Arg Arg Pro Trp
            325                 330                 335
Trp Pro Cys Arg Ile Cys Ser Asp Pro Leu Ile Asn Thr His Ser Lys
            340                 345                 350
Met Lys Val Ser Asn Arg Arg Pro Tyr Arg Gln Tyr Tyr Val Glu Ala
            355                 360                 365
Phe Gly Asp Pro Ser Glu Arg Ala Trp Val Ala Gly Lys Ala Ile Val
    370                 375                 380
Met Phe Glu Gly Arg His Gln Phe Glu Glu Leu Pro Val Leu Arg Arg
385             390                 395                 400
Arg Gly Lys Gln Lys Glu Lys Gly Tyr Arg His Lys Val Pro Gln Lys
            405                 410                 415
Ile Leu Ser Lys Trp Glu Ala Ser Val Gly Leu Ala Glu Gln Tyr Asp
            420                 425                 430
Val Pro Lys Gly Ser Lys Asn Arg Lys Cys Ile Pro Gly Ser Ile Lys
            435                 440                 445
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Leu Asp Ser Glu Glu Asp Met Pro Phe Glu Asp Cys Thr Asn Asp Pro
    450   455   460
Glu Ser Glu His Asp Leu Leu Leu Asn Gly Cys Leu Lys Ser Leu Ala
465   470   475   480
Phe Asp Ser Glu His Ser Ala Asp Glu Lys Glu Lys Pro Cys Ala Lys
                485   490   495
Ser Arg Ala Arg Lys Ser Ser Asp Asn Pro Lys Arg Thr Ser Val Lys
            500   505   510
Lys Gly His Ile Gln Phe Glu Ala His Lys Asp Glu Arg Arg Gly Lys
            515   520   525
Ile Pro Glu Asn Leu Gly Leu Asn Phe Ile Ser Gly Asp Ile Ser Asp
    530   535   540
Thr Gln Ala Ser Asn Glu Leu Ser Arg Ile Ala Asn Ser Leu Thr Gly
545   550   555   560
Ser Asn Thr Ala Pro Gly Ser Phe Leu Phe Ser Ser Cys Gly Lys Asn
            565   570   575
Thr Ala Lys Lys Glu Phe Glu Thr Ser Asn Gly Asp Ser Leu Leu Gly
            580   585   590
Leu Pro Glu Gly Ala Leu Ile Ser Lys Cys Ser Arg Glu Lys Asn Lys
        595   600   605
Pro Gln Arg Ser Leu Val Cys Gly Ser Lys Val Lys Leu Cys Tyr Ile
    610   615   620
Gly Ala Gly Asp Glu Glu Lys Arg Ser Asp Ser Ile Ser Ile Cys Thr
625   630   635   640
Thr Ser Asp Asp Gly Ser Ser Asp Leu Asp Pro Ile Glu His Ser Ser
            645   650   655
Glu Ser Asp Asn Ser Val Leu Glu Ile Pro Asp Ala Phe Asp Arg Thr
            660   665   670
Glu Asn Met Leu Ser Met Gln Lys Asn Glu Lys Ile Lys Tyr Ser Arg
            675   680   685
Phe Ala Ala Thr Asn Thr Arg Val Lys Ala Lys Gln Lys Pro Leu Ile
    690   695   700
Ser Asn Ser His Thr Asp His Leu Met Gly Cys Thr Lys Ser Ala Glu
705   710   715   720
Pro Gly Thr Glu Thr Ser Gln Val Asn Leu Ser Asp Leu Lys Ala Ser
            725   730   735
Thr Leu Val His Lys Pro Gln Ser Asp Phe Thr Asn Asp Ala Leu Ser
            740   745   750
Pro Lys Phe Asn Leu Ser Ser Ser Ile Ser Ser Glu Asn Ser Leu Ile
    755   760   765
Lys Gly Gly Ala Ala Asn Gln Ala Leu Leu His Ser Lys Ser Lys Gln
    770   775   780
Pro Lys Phe Arg Ser Ile Lys Cys Lys His Lys Glu Asn Pro Val Met
785   790   795   800
Ala Glu Pro Pro Val Ile Asn Glu Glu Cys Ser Leu Lys Cys Cys Ser
            805   810   815
Ser Asp Thr Lys Gly Ser Pro Leu Ala Ser Ile Ser Lys Ser Gly Lys
            820   825   830
Val Asp Gly Leu Lys Leu Leu Asn Asn Met His Glu Lys Thr Arg Asp
        835   840   845
Ser Ser Asp Ile Glu Thr Ala Val Val Lys His Val Leu Ser Glu Leu
850   855   860
Lys Glu Leu Ser Tyr Arg Ser Leu Gly Glu Asp Val Ser Asp Ser Gly
865   870   875   880
Thr Ser Lys Pro Ser Lys Pro Leu Leu Phe Ser Ser Ala Ser Ser Gln
            885   890   895
Asn His Ile Pro Ile Glu Pro Asp Tyr Lys Phe Ser Thr Leu Leu Met
        900   905   910
Met Leu Lys Asp Met His Asp Ser Lys Thr Lys Glu Gln Arg Leu Met
    915   920   925

59

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Thr Ala Gln Asn Leu Val Ser Tyr Arg Ser Pro Gly Arg Gly Asp Cys
    930                     935                 940
Ser Thr Asn Ser Pro Val Gly Val Ser Lys Val Leu Val Ser Gly Gly
945                     950                 955                 960
Ser Thr His Asn Ser Glu Lys Lys Gly Asp Gly Thr Gln Asn Ser Ala
                965                 970                 975
Asn Pro Ser Pro Ser Gly Gly Asp Ser Ala Leu Ser Gly Glu Leu Ser
                980                 985                 990
Ala Ser Leu Pro Gly Leu Leu Ser Asp Lys Arg Asp Leu Pro Ala Ser
        995             .   1000                1005
Gly Lys Ser Arg Ser Asp Cys Val Thr Arg Arg Asn Cys Gly Arg Ser
        1010                1015                1020
Lys Pro Ser Ser Lys Leu Arg Asp Ala Phe Ser Ala Gln Met Val Lys
1025                1030                1035                1040
Asn Thr Val Asn Arg Lys Ala Leu Lys Thr Glu Arg Lys Arg Lys Leu
                1045                1050                1055
Asn Gln Leu Pro Ser Val Thr Leu Asp Ala Val Leu Gln Gly Asp Arg
            1060                1065                1070
Glu Arg Gly Gly Ser Leu Arg Gly Gly Ala Glu Asp Pro Ser Lys Glu
        1075                1080                1085
Asp Pro Leu Gln Ile Met Gly His Leu Thr Ser Glu Asp Gly Asp His
    1090                1095                1100
Phe Ser Asp Val His Phe Asp Ser Lys Val Lys Gln Ser Asp Pro Gly
1105                1110                1115                1120
Lys Ile Ser Glu Lys Gly Leu Ser Phe Glu Asn Gly Lys Gly Pro Glu
                1125                1130                1135
Leu Asp Ser Val Met Asn Ser Glu Asn Asp Glu Leu Asn Gly Val Asn
            1140                1145                1150
Gln Val Val Pro Lys Lys Arg Trp Gln Arg Leu Asn Gln Arg Arg Thr
        1155                1160                1165
Lys Pro Arg Lys Arg Met Asn Arg Phe Lys Glu Lys Glu Asn Ser Glu
    1170                1175                1180
Cys Ala Phe Arg Val Leu Leu Pro Ser Asp Pro Val Gln Glu Gly Arg
1185                1190                1195                1200
Asp Glu Phe Pro Glu His Arg Thr Pro Ser Ala Ser Ile Leu Glu Glu
            1205             .   1210                1215
Pro Leu Thr Glu Gln Asn His Ala Asp Cys Leu Asp Ser Ala Gly Pro
            1220                1225                1230
Arg Leu Asn Val Cys Asp Lys Ser Ser Ala Ser Ile Gly Asp Met Glu
        1235                1240                1245
Lys Glu Pro Gly Ile Pro Ser Leu Thr Pro Gln Ala Glu Leu Pro Glu
    1250                1255                1260
Pro Ala Val Arg Ser Glu Lys Lys Arg Leu Arg Lys Pro Ser Lys Trp
1265                1270                1275                1280
Leu Leu Glu Tyr Thr Glu Glu Tyr Asp Gln Ile Phe Ala Pro Lys Lys
            1285                1290                1295
Lys Gln Lys Lys Val Gln Glu Gln Val His Lys Val Ser Ser Arg Cys
        1300                1305                1310
Glu Glu Glu Ser Leu Leu Ala Arg Gly Arg Ser Ser Ala Gln Asn Lys
        1315                1320                1325
Gln Val Asp Glu Asn Ser Leu Ile Ser Thr Lys Glu Glu Pro Pro Val
    1330                1335                1340
Leu Glu Arg Glu Ala Pro Phe Leu Glu Gly Pro Leu Ala Gln Ser Glu
1345                1350                1355                1360
Leu Gly Gly Gly His Ala Glu Leu Pro Gln Leu Thr Leu Ser Val Pro
            1365                1370                1375
Val Ala Pro Glu Val Ser Pro Arg Pro Ala Leu Glu Ser Glu Glu Leu
        1380                1385                1390
Leu Val Lys Thr Pro Gly Asn Tyr Glu Ser Lys Arg Gln Arg Lys Pro
    1395                1400                1405
```

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Thr Lys Lys Leu Leu Glu Ser Asn Asp Leu Asp Pro Gly Phe Met Pro
    1410                1415                1420
Lys Lys Gly Asp Leu Gly Leu Ser Lys Lys Cys Tyr Glu Ala Gly His
1425                1430                1435                1440
Leu Glu Asn Gly Ile Thr Glu Ser Cys Ala Thr Ser Tyr Ser Lys Asp
                1445                1450                1455
Phe Gly Gly Gly Thr Thr Lys Ile Phe Asp Lys Pro Arg Lys Arg Lys
                1460                1465                1470
Arg Gln Arg His Ala Ala Ala Lys Met Gln Cys Lys Lys Val Lys Asn
            1475                1480                1485
Asp Asp Ser Ser Lys Glu Ile Pro Gly Ser Glu Gly Glu Leu Met Pro
    1490                1495                1500
His Arg Thr Ala Thr Ser Pro Lys Glu Thr Val Glu Glu Gly Val Glu
1505                1510                1515                1520
His Asp Pro Gly Met Pro Ala Ser Lys Lys Met Gln Gly Glu Arg Gly
                1525                1530                1535
Gly Gly Ala Ala Leu Lys Glu Asn Val Cys Gln Asn Cys Glu Lys Leu
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Gly Glu Leu Leu Leu Cys Glu Ala Gln Cys Cys Gly Ala Phe His Leu
            1555                1560                1565
Glu Cys Leu Gly Leu Thr Glu Met Pro Arg Gly Lys Phe Ile Cys Asn
    1570                1575                1580
Glu Cys Arg Thr Gly Ile His Thr Cys Phe Val Cys Lys Gln Ser Gly
1585                1590                1595                1600
Glu Asp Val Lys Arg Cys Leu Leu Pro Leu Cys Gly Lys Phe Tyr His
                1605                1610                1615
Glu Glu Cys Val Gln Lys Tyr Pro Pro Thr Val Met Gln Asn Lys Gly
                1620                1625                1630
Phe Arg Cys Ser Leu His Ile Cys Ile Thr Cys His Ala Ala Asn Pro
            1635                1640                1645
Ala Asn Val Ser Ala Ser Lys Gly Arg Leu Met Arg Cys Val Arg Cys
    1650                1655                1660
Pro Val Ala Tyr His Ala Asn Asp Phe Cys Leu Ala Ala Gly Ser Lys
1665                1670                1675                1680
Ile Leu Ala Ser Asn Ser Ile Ile Cys Pro Asn His Phe Thr Pro Arg
                1685                1690                1695
Arg Gly Cys Arg Asn His Glu His Val Asn Val Ser Trp Cys Phe Val
            1700                1705                1710
Cys Ser Glu Gly Gly Ser Leu Leu Cys Cys Asp Ser Cys Pro Ala Ala
            1715                1720                1725
Phe His Arg Glu Cys Leu Asn Ile Asp Ile Pro Glu Gly Asn Trp Tyr
    1730                1735                1740
Cys Asn Asp Cys Lys Ala Gly Lys Lys Pro His Tyr Arg Glu Ile Val
1745                1750                1755                1760
Trp Val Lys Val Gly Arg Tyr Arg Trp Trp Pro Ala Glu Ile Cys His
                1765                1770                1775
Pro Arg Ala Val Pro Ser Asn Ile Asp Lys Met Arg His Asp Val Gly
            1780                1785                1790
Glu Phe Pro Val Leu Phe Phe Gly Ser Asn Asp Tyr Leu Trp Thr His
            1795                1800                1805
Gln Ala Arg Val Phe Pro Tyr Met Glu Gly Asp Val Ser Ser Lys Asp
    1810                1815                1820
Lys Met Gly Lys Gly Val Asp Gly Thr Tyr Lys Lys Ala Leu Gln Glu
1825                1830                1835                1840
Ala Ala Ala Arg Phe Glu Glu Leu Lys Ala Gln Lys Glu Leu Arg Gln
                1845                1850                1855
Leu Gln Glu Asp Arg Lys Asn Asp Lys Lys Pro Pro Pro Tyr Lys His
            1860                1865                1870
Ile Lys Val Asn Arg Pro Ile Gly Arg Val Gln Ile Phe Thr Ala Asp
    1875                1880                1885
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Leu Ser Glu Ile Pro Arg Cys Asn Cys Lys Ala Thr Asp Glu Asn Pro
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Cys Gly Ile Asp Ser Glu Cys Ile Asn Arg Met Leu Leu Tyr Glu Cys
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His Pro Thr Val Cys Pro Ala Gly Gly Arg Cys Gln Asn Gln Cys Phe
            1925            1930            1935
Ser Lys Arg Gln Tyr Pro Glu Val Glu Ile Phe Arg Thr Leu Gln Arg
        1940            1945            1950
Gly Trp Gly Leu Arg Thr Lys Thr Asp Ile Lys Lys Gly Glu Phe Val
        1955            1960            1965
Asn Glu Tyr Val Gly Glu Leu Ile Asp Glu Glu Glu Cys Arg Ala Arg
    1970            1975            1980
Ile Arg Tyr Ala Gln Glu His Asp Ile Thr Asn Phe Tyr Met Leu Thr
1985            1990            1995            2000
Leu Asp Lys Asp Arg Ile Ile Asp Ala Gly Pro Lys Gly Asn Tyr Ala
            2005            2010            2015
Arg Phe Met Asn His Cys Cys Gln Pro Asn Cys Glu Thr Gln Lys Trp
        2020            2025            2030
Ser Val Asn Gly Asp Thr Arg Val Gly Leu Phe Ala Leu Ser Asp Ile
        2035            2040            2045
Lys Ala Gly Thr Glu Leu Thr Phe Asn Tyr Asn Leu Glu Cys Leu Gly
    2050            2055            2060
Asn Gly Lys Thr Val Cys Lys Cys Gly Ala Pro Asn Cys Ser Gly Phe
2065            2070            2075            2080
Leu Gly Val Arg Pro Lys Asn Gln Pro Ile Ala Thr Glu Glu Lys Ser
            2085            2090            2095
Lys Lys Phe Lys Lys Lys Gln Gln Gly Lys Arg Arg Thr Gln Gly Glu
            2100            2105            2110
Ile Thr Lys Glu Arg Glu Asp Glu Cys Phe Ser Cys Gly Asp Ala Gly
        2115            2120            2125
Gln Leu Val Ser Cys Lys Lys Pro Gly Cys Pro Lys Val Tyr His Ala
    2130            2135            2140
Asp Cys Leu Asn Leu Thr Lys Arg Pro Ala Gly Lys Trp Glu Cys Pro
2145            2150            2155            2160
Trp His Gln Cys Asp Ile Cys Gly Lys Glu Ala Ala Ser Phe Cys Glu
            2165            2170            2175
Met Cys Pro Ser Ser Phe Cys Lys Gln His Arg Glu Gly Met Leu Phe
        2180            2185            2190
Ile Ser Lys Leu Asp Gly Arg Leu Ser Cys Thr Glu His Asp Pro Cys
        2195            2200            2205
Gly Pro Asn Pro Leu Glu Pro Gly Glu Ile Arg Glu Tyr Val Pro Pro
    2210            2215            2220
Pro Val Pro Leu Pro Pro Gly Pro Ser Thr His Leu Ala Glu Gln Ser
2225            2230            2235            2240
Thr Gly Met Ala Ala Gln Ala Pro Lys Met Ser Asp Lys Pro Pro Ala
            2245            2250            2255
Asp Thr Asn Gln Met Leu Ser Leu Ser Lys Lys Ala Leu Ala Gly Thr
        2260            2265            2270
Cys Gln Arg Pro Leu Leu Pro Glu Arg Pro Leu Glu Arg Thr Asp Ser
        2275            2280            2285
Arg Pro Gln Pro Leu Asp Lys Val Arg Asp Leu Ala Gly Ser Gly Thr
    2290            2295            2300
Lys Ser Gln Ser Leu Val Ser Ser Gln Arg Pro Leu Asp Arg Pro Pro
2305            2310            2315            2320
Ala Val Ala Gly Pro Arg Pro Gln Leu Ser Asp Lys Pro Ser Pro Val
            2325            2330            2335
Thr Ser Pro Ser Ser Ser Pro Ser Val Arg Ser Gln Pro Leu Glu Arg
        2340            2345            2350
Pro Leu Gly Thr Ala Asp Pro Arg Leu Asp Lys Ser Ile Gly Ala Ala
    2355            2360            2365
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Ser Pro Arg Pro Gln Ser Leu Glu Lys Thr Ser Val Pro Thr Gly Leu
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Arg Leu Pro Pro Pro Asp Arg Leu Leu Ile Thr Ser Ser Pro Lys Pro
2385              2390              2395              2400
Gln Thr Ser Asp Arg Pro Thr Asp Lys Pro His Ala Ser Leu Ser Gln
              2405              2410              2415
Arg Leu Pro Pro Pro Glu Lys Val Leu Ser Ala Val Val Gln Thr Leu
              2420              2425              2430
Val Ala Lys Glu Lys Ala Leu Arg Pro Val Asp Gln Asn Thr Gln Ser
              2435              2440              2445
Lys Asn Arg Ala Ala Leu Val Met Asp Leu Ile Asp Leu Thr Pro Arg
              2450              2455              2460
Gln Lys Glu Arg Ala Ala Ser Pro His Gln Val Thr Pro Gln Ala Asp
2465              2470              2475              2480
Glu Lys Met Pro Val Leu Glu Ser Ser Ser Trp Pro Ala Ser Lys Gly
              2485              2490              2495
Leu Gly His Met Pro Arg Ala Val Glu Lys Gly Cys Val Ser Asp Pro
              2500              2505              2510
Leu Gln Thr Ser Gly Lys Ala Ala Ala Pro Ser Glu Asp Pro Trp Gln
              2515              2520              2525
Ala Val Lys Ser Leu Thr Gln Ala Arg Leu Leu Ser Gln Pro Pro Ala
              2530              2535              2540
Lys Ala Phe Leu Tyr Glu Pro Thr Thr Gln Ala Ser Gly Arg Ala Ser
2545              2550              2555              2560
Ala Gly Ala Glu Gln Thr Pro Gly Pro Leu Ser Gln Ser Pro Gly Leu
              2565              2570              2575
Val Lys Gln Ala Lys Gln Met Val Gly Gly Gln Gln Leu Pro Ala Leu
              2580              2585      ·        2590
Ala Ala Lys Ser Gly Gln Ser Phe Arg Ser Leu Gly Lys Ala Pro Ala
              2595              2600              2605
Ser Leu Pro Thr Glu Glu Lys Lys Leu Val Thr Thr Glu Gln Ser Pro
    2610              2615              2620
Trp Ala Leu Gly Lys Ala Ser Ser Arg Ala Gly Leu Trp Pro Ile Val
2625              2630              2635              2640
Ala Gly Gln Thr Leu Ala Gln Ser Cys Trp Ser Ala Gly Ser Thr Gln
              2645              2650              2655
Thr Leu Ala Gln Thr Cys Trp Ser Leu Gly Arg Gly Gln Asp Pro Lys
              2660              2665              2670
Pro Glu Gln Asn Thr Leu Pro Ala Leu Asn Gln Ala Pro Ser Ser His
    2675              2680              2685
Lys Cys Ala Glu Ser Glu Gln Lys
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ggtcaatcca atttttctga gccacttaat gggtgtacta tgcagttatc gactgtcagt     180
ggaacatccc aaaatgctta tggacaagat tctccatctt gttacattcc actgcggaga     240
ctacaggatt tggcctccat gatcaatgta gagtatttaa atgggtctgc tgatggatca     300
gaatcctttc aagaccctga aaaaagtgat tcaagagctc agacgccaat gtttgcact      360
tccttgagtc ctggtggtcc tacagcactt gctatgaaac aggaaccctc ttgtaataac     420
tcccctgaac tccaggtaaa agtaacaaag actatcaaga atggctttct gcactttgag     480
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ccagagagta gacacggtgc agtcaaatcg ccattcttgc cattagctcc tcagactgaa   720
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ggggcttatg gttgtgtgaa ccatgtatga aaatccagtg ggccccaacc aaggagacag    8340
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<210> 38
<211> 1784
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 38
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Arg Leu Leu Glu Glu Asp Thr Pro Arg Tyr Met Arg Ala Ser Asp Pro
            35                  40                  45
Ala Ser Pro His Ile Gly Arg Ser Asn Glu Glu Glu Glu Thr Ser Asp
        50                  55                  60
Ser Ser Leu Glu Lys Gln Thr Arg Ser Lys Tyr Cys Thr Glu Thr Ser
65                  70                  75                  80
Gly Val His Gly Asp Ser Pro Tyr Gly Ser Gly Thr Met Asp Thr His
                85                  90                  95
Ser Leu Glu Ser Lys Ala Glu Arg Ile Ala Arg Tyr Lys Ala Glu Arg
            100                 105                 110
Arg Arg Gln Leu Ala Glu Lys Tyr Gly Leu Thr Leu Asp Pro Glu Ala
        115                 120                 125
Asp Ser Glu Tyr Leu Ser Arg Tyr Thr Lys Ser Arg Lys Glu Pro Asp
    130                 135                 140
Ala Val Glu Lys Arg Gly Gly Lys Ser Asp Lys Gln Glu Glu Ser Ser
145                 150                 155                 160
Arg Asp Ala Ser Ser Leu Tyr Pro Gly Thr Glu Thr Met Gly Leu Arg
                165                 170                 175
Thr Cys Ala Gly Glu Ser Lys Asp Tyr Ala Leu His Ala Gly Asp Gly
            180                 185                 190
Ser Ser Asp Pro Glu Val Leu Leu Asn Ile Glu Asn Gln Arg Arg Gly
        195                 200                 205
Gln Glu Leu Ser Ala Thr Arg Gln Ala His Asp Leu Ser Pro Ala Ala
    210                 215                 220
Glu Ser Ser Ser Thr Phe Ser Phe Ser Gly Arg Asp Ser Ser Phe Thr
225                 230                 235                 240
Glu Val Pro Arg Ser Pro Lys His Ala His Ser Ser Ser Leu Gln Gln
                245                 250                 255
Ala Ala Ser Arg Ser Pro Ser Phe Gly Asp Pro Gln Leu Ser Pro Glu
            260                 265                 270
Ala Arg Pro Arg Cys Thr Ser His Ser Glu Thr Pro Thr Val Asp Asp
        275                 280                 285
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Glu Glu Lys Val Asp Glu Arg Ala Lys Leu Ser Val Ala Ala Lys Arg
    290                 295                 300
Leu Leu Phe Arg Glu Met Glu Lys Ser Phe Asp Glu Gln Asn Val Pro
305                 310                 315                 320
Lys Arg Arg Ser Arg Asn Thr Ala Val Glu Gln Arg Leu Arg Arg Leu
                325                 330                 335    .
Gln Asp Arg Ser Leu Thr Gln Pro Ile Thr Thr Glu Glu Val Val Ile
                340                 345                 350
Ala Ala Thr Leu Gln Ala Ser Ala His Gln Lys Ala Leu Ala Lys Asp
            355                 360                 365
Gln Thr Asn Glu Gly Lys Glu Leu Ala Glu Gln Gly Glu Pro Asp Ser
    370                 375                 380
Ser Thr Leu Ser Leu Ala Glu Lys Leu Ala Leu Phe Asn Lys Leu Ser
385             390                 395                 400
Gln Pro Val Ser Lys Ala Ile Ser Thr Arg Asn Arg Ile Asp Thr Arg
                405                 410                 415
Gln Arg Arg Met Asn Ala Arg Tyr Gln Thr Gln Pro Val Thr Leu Gly
                420                 425                 430
Glu Val Glu Gln Val Gln Ser Gly Lys Leu Ile Pro Phe Ser Pro Ala
        435                 440                 445
Val Asn Thr Ser Val Ser Thr Val Ala Ser Thr Val Ala Pro Met Tyr
    450                 455                 460
Ala Gly Asp Leu Arg Thr Lys Pro Pro Leu Asp His Asn Ala Ser Ala
465             470                 475                 480
Thr Asp Tyr Lys Phe Ser Ser Ser Ile Glu Asn Ser Asp Ser Pro Val
                485                 490                 495
Arg Ser Ile Leu Lys Ser Gln Ala Trp Gln Pro Leu Val Glu Gly Ser
            500                 505                 510
Glu Asn Lys Gly Met Leu Arg Glu Tyr Gly Glu Thr Glu Ser Lys Arg
    515                 520                 525
Ala Leu Thr Gly Arg Asp Ser Gly Met Glu Lys Tyr Gly Ser Phe Glu
    530                 535                 540
Glu Ala Glu Ala Ser Tyr Pro Ile Leu Asn Arg Ala Arg Glu Gly Asp
545             550                 555                 560
Ser His Lys Glu Ser Lys Tyr Ala Val Pro Arg Arg Gly Ser Leu Glu
                565                 570                 575
Arg Ala Asn Pro Pro Ile Thr His Leu Gly Asp Glu Pro Lys Glu Phe
            580                 585                 590
Ser Met Ala Lys Met Asn Ala Gln Gly Asn Leu Asp Leu Arg Asp Arg
`   595                 600                 605
Leu Pro Phe Glu Glu Lys Val Glu Val Glu Asn Val Met Lys Arg Lys
    610                 615                 620
Phe Ser Leu Arg Ala Ala Glu Phe Gly Glu Pro Thr Ser Glu Gln Thr
625             630                 635                 640
Gly Thr Ala Ala Gly Lys Thr Ile Ala Gln Thr Thr Ala Pro Val Ser
            645                 650                 655
Trp Lys Pro Gln Asp Ser Ser Glu Gln Pro Gln Glu Lys Leu Cys Lys
                660                 665                 670
Asn Pro Cys Ala Met Phe Ala Ala Gly Glu Ile Lys Thr Pro Thr Gly
        675                 680                 685
Glu Gly Leu Leu Asp Ser Pro Ser Lys Thr Met Ser Ile Lys Glu Arg
    690                 695                 700
Leu Ala Leu Leu Lys Lys Ser Gly Glu Glu Asp Trp Arg Asn Arg Leu
705             710                 715                 720
Ser Arg Arg Gln Glu Gly Gly Lys Ala Pro Ala Ser Ser Leu His Thr
                725                 730                 735
Gln Glu Ala Gly Arg Ser Leu Ile Lys Lys Arg Val Thr Glu Ser Arg
            740                 745                 750
Glu Ser Gln Met Thr Ile Glu Glu Arg Lys Gln Leu Ile Thr Val Arg
    755                 760                 765
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Glu Glu Ala Trp Lys Thr Arg Gly Arg Gly Ala Ala Asn Asp Ser Thr
    770                 775                 780
Gln Phe Thr Val Ala Gly Arg Met Val Lys Lys Gly Leu Ala Ser Pro
785                 790                 795                 800
Thr Ala Ile Thr Pro Val Ala Ser Ala Ile Cys Gly Lys Thr Arg Gly
            805                 810                 815
Thr Thr Pro Val Ser Lys Pro Leu Glu Asp Ile Glu Ala Arg Pro Asp
            820                 825                 830
Met Gln Leu Glu Ser Asp Leu Lys Leu Asp Arg Leu Glu Thr Phe Leu
            835                 840                 845
Arg Arg Leu Asn Asn Lys Val Gly Gly Met His Glu Thr Val Leu Thr
    850                 855                 860
Val Thr Gly Lys Ser Val Lys Glu Val Met Lys Pro Asp Asp Asp Glu
865                 870                 875                 880
Thr Phe Ala Lys Phe Tyr Arg Ser Val Asp Tyr Asn Met Pro Arg Ser
                885                 890                 895
Pro Val Glu Met Asp Glu Asp Phe Asp Val Ile Phe Asp Pro Tyr Ala
            900                 905                 910
Pro Lys Leu Thr Ser Ser Val Ala Glu His Lys Arg Ala Val Arg Pro
    915                 920                 925
Lys Arg Arg Val Gln Ala Ser Lys Asn Pro Leu Lys Met Leu Ala Ala
    930                 935                 940
Arg Glu Asp Leu Leu Gln Glu Tyr Thr Glu Gln Arg Leu Asn Val Ala
945                 950                 955                 960
Phe Met Glu Ser Lys Arg Met Lys Val Glu Lys Met Ser Ser Asn Ser
                965                 970                 975
Asn Phe Ser Glu Val Thr Leu Ala Gly Leu Ala Ser Lys Glu Asn Phe
            980                 985                 990
Ser Asn Val Ser Leu Arg Ser Val Asn Leu Thr Glu Gln Asn Ser Asn
    995                 1000                1005
Asn Ser Ala Val Pro Tyr Lys Arg Leu Met Leu Leu Gln Ile Lys Gly
    1010                1015                1020
Arg Arg His Val Gln Thr Arg Leu Val Glu Pro Arg Ala Ser Ala Leu
1025                1030                1035                1040
Asn Ser Gly Asp Cys Phe Leu Leu Leu Ser Pro His Cys Cys Phe Leu
            1045                1050                1055
Trp Val Gly Glu Phe Ala Asn Val Ile Glu Lys Ala Lys Ala Ser Glu
            1060                1065                1070
Leu Ala Thr Leu Ile Gln Thr Lys Arg Glu Leu Gly Cys Arg Ala Thr
    1075                1080                1085
Tyr Ile Gln Thr Ile Glu Glu Gly Ile Asn Thr His Thr His Ala Ala
    1090                1095                1100
Lys Asp Phe Trp Lys Leu Leu Gly Gly Gln Thr Ser Tyr Gln Ser Ala
1105                1110                1115                1120
Gly Asp Pro Lys Glu Asp Glu Leu Tyr Glu Ala Ala Ile Ile Glu Thr
            1125                1130                1135
Asn Cys Ile Tyr Arg Leu Met Asp Asp Lys Leu Val Pro Asp Asp Asp
            1140                1145                1150
Tyr Trp Gly Lys Ile Pro Lys Cys Ser Leu Leu Gln Pro Lys Glu Val
    1155                1160                1165
Leu Val Phe Asp Phe Gly Ser Glu Val Tyr Val Trp His Gly Lys Glu
    1170                1175                1180
Val Thr Leu Ala Gln Arg Lys Ile Ala Phe Gln Leu Ala Lys His Leu
1185                1190                1195                1200
Trp Asn Gly Thr Phe Asp Tyr Glu Asn Cys Asp Ile Asn Pro Leu Asp
            1205                1210                1215
Pro Gly Glu Cys Asn Pro Leu Ile Pro Arg Lys Gly Gln Gly Arg Pro
            1220                1225                1230
Asp Trp Ala Ile Phe Gly Arg Leu Thr Glu His Asn Glu Thr Ile Leu
    1235                1240                1245
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Phe Lys Glu Lys Phe Leu Asp Trp Thr Glu Leu Lys Arg Ser Asn Glu
    1250                1255                1260
Lys Asn Pro Gly Glu Leu Ala Gln His Lys Glu Asp Pro Arg Thr Asp
1265                1270                1275                1280
Val Lys Ala Tyr Asp Val Thr Arg Met Val Ser Met Pro Gln Thr Thr
                1285                1290                1295
Ala Gly Thr Ile Leu Asp Gly Val Asn Val Gly Arg Gly Tyr Gly Leu
            1300                1305                1310
Val Glu Gly His Asp Arg Arg Gln Phe Glu Ile Thr Ser Val Ser Val
            1315                1320                1325
Asp Val Trp His Ile Leu Glu Phe Asp Tyr Ser Arg Leu Pro Lys Gln
        1330                1335                1340
Ser Ile Gly Gln Phe His Glu Gly Asp Ala Tyr Val Val Lys Trp Lys
1345                1350                1355                1360
Phe Met Val Ser Thr Ala Val Gly Ser Arg Gln Lys Gly Glu His Ser
                1365                1370                1375
Val Arg Ala Ala Gly Lys Glu Lys Cys Val Tyr Phe Phe Trp Gln Gly
            1380                1385                1390
Arg His Ser Thr Val Ser Glu Lys Gly Thr Ser Ala Leu Met Thr Val
            1395                1400                1405
Glu Leu Asp Glu Glu Arg Gly Ala Gln Val Gln Val Leu Gln Gly Lys
        1410                1415                1420
Glu Pro Pro Cys Phe Leu Gln Cys Phe Gln Gly Gly Met Val Val His
1425                1430                1435                1440
Ser Gly Arg Arg Glu Glu Glu Glu Glu Asn Val Gln Ser Glu Trp Arg
                1445                1450                1455
Leu Tyr Cys Val Arg Gly Glu Val Pro Val Glu Gly Asn Leu Leu Glu
            1460                1465                1470
Val Ala Cys His Cys Ser Ser Leu Arg Ser Arg Thr Ser Met Val Val
            1475                1480                1485
Leu Asn Val Asn Lys Ala Leu Ile Tyr Leu Trp His Gly Cys Lys Ala
        1490                1495                1500
Gln Ala His Thr Lys Glu Val Gly Arg Thr Ala Ala Asn Lys Ile Lys
1505                1510                1515                1520
Glu Gln Cys Pro Leu Glu Ala Gly Leu His Ser Ser Ser Lys Val Thr
                1525                1530                1535
Ile His Glu Cys Asp Glu Gly Ser Glu Pro Leu Gly Phe Trp Asp Ala
            1540                1545                1550
Leu Gly Arg Arg Asp Arg Lys Ala Tyr Asp Cys Met Leu Gln Asp Pro
        1555                1560                1565
Gly Ser Phe Asn Phe Ala Pro Arg Leu Phe Ile Leu Ser Ser Ser Ser
    1570                1575                1580
Gly Asp Phe Ala Ala Thr Glu Phe Val Tyr Pro Ala Arg Ala Pro Ser
1585                1590                1595                1600
Val Val Ser Ser Met Pro Phe Leu Gln Glu Asp Leu Tyr Ser Ala Pro
                1605                1610                1615
Gln Pro Ala Leu Phe Leu Val Asp Asn His His Glu Val Tyr Leu Trp
        1620                1625                1630
Gln Gly Trp Trp Pro Ile Glu Asn Lys Ile Thr Gly Ser Ala Arg Ile
        1635                1640                1645
Arg Trp Ala Ser Asp Arg Lys Ser Ala Met Glu Thr Val Leu Gln Tyr
    1650                1655                1660
Cys Lys Gly Lys Asn Leu Lys Lys Pro Ala Pro Lys Ser Tyr Leu Ile
1665                1670                1675                1680
His Ala Gly Leu Glu Pro Leu Thr Phe Thr Asn Met Phe Pro Ser Trp
                1685                1690                1695
Glu His Arg Glu Asp Ile Ala Glu Ile Thr Glu Met Asp Thr Glu Val
            1700                1705                1710
Ser Asn Gln Ile Thr Leu Val Glu Asp Val Leu Ala Lys Leu Cys Lys
        1715                1720                1725
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Thr Ile Tyr Pro Leu Ala Asp Leu Leu Ala Arg Pro Leu Pro Glu Gly
    1730                1735                1740
Val Asp Pro Leu Lys Leu Glu Ile Tyr Leu Thr Asp Glu Asp Phe Glu
1745                1750                1755                1760
Phe Ala Leu Asp Met Thr Arg Asp Glu Tyr Asn Ala Leu Pro Ala Trp
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Lys Gln Val Asn Leu Lys Lys Ala
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<210> 39
<211> 6719
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

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ctcactgagt tttgactagc ggaagaaaag agagagttca agtggatggc cttgaggact     180
tgaaaagctg agatatgatg attttgaagt catttcacat cgaagccatg atttaaatat     240
cggcgttaag atttcaacaa gaaaaactta agcttccttg gattcccacg tcaaaggaaa     300
gtttcaagct ttcagaagga gttctcactc gaagataaag aacagctcgc taaccacgaa     360
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tttgaaccaa agaagaaaga attcttagaa atgaaaagaa agaaagaat tgccaggcgc      480
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ggtaccatgg acacccacag tctggagtcc aaagccgaaa gaattgcaag gtacaaagca     780
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accacagccc ccgtgtcctg gaagccccag gattcttcgg aacagccaca ggagaagctc    2460
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tggcacatcc tggaattcga ctatagcagg ctccccaaac aaagcatcgg gcagttccat   4500
gagggggatg cctatgtggt caagtggaag ttcatggtga gcacggcagt gggaagtcgc   4560
cagaagggag agcactcggt gagggcagcc ggcaaagaga agtgcgtcta cttcttctgg   4620
caaggccggc actccaccgt gagtgagaag ggcacgtcgg cgctgatgac ggtggagctg   4680
gacgaggaaa gggggggccca ggtccaggtt ctccagggaa aggagccccc ctgtttcctg   4740
cagtgtttcc aggggggggat ggtggtgcac tcggggaggc gggaagagga agaagaaaat   4800
gtgcaaagtg agtggcggct gtactgcgtg cgtggagagg tgcccgtgga agggaatttg   4860
ctggaagtgg cctgtcactg tagcagcctg aggtccagaa cttccatggt ggtgcttaac   4920
gtcaacaagg ccctcatcta cctgtggcac ggatgcaaag cccaggccca cacgaaggag   4980
gtcggaagga ccgctgcgaa caagatcaag gaacaatgtc ccctggaagc aggactgcat   5040
agtagcagca aagtcacaat acacgagtgt gatgaaggct ccgagccact cggattctgg   5100
gatgccttag aaggagaga caggaaagcc tacgattgca tgcttcaaga tcctggaagt   5160
tttaacttcg cgccccgcct gttcatcctc agcagctcct ctggggattt tgcagccaca   5220
gagtttgtgt accctgcccg agccccctct gtggtcagtt ccatgccctt cctgcaggaa   5280
gatctgtaca gcgcgcccca gccagcactt ttccttgttg acaatcacca cgaggtgtac   5340
ctctggcaag gctggtggcc catcgagaac aagatcactg gttccgcccg catccgctgg   5400
gcctccgacc ggaagagtgc gatggagact gtgctccagt actgcaaagg aaaaaatctc   5460
aagaaaccag ccccaagtc ttaccttatc cacgctggtc tggagccccct gacattcacc   5520
aatatgtttc ccagctggga gcacagagag gacatcgctg agatcacaga gatggacacg   5580
gaagtttcca atcagatcac cctcgtggaa gacgtcttag ccaagctctg taaaaccatt   5640
tacccgctgg ccgacctcct ggccaggcca ctcccggagg gggtcgatcc tctgaagctt   5700
gagatctatc tcaccgacga agacttcgag tttgcactag acatgacgag ggatgaatac   5760
aacgccctgc ccgcctggaa gcaggtgaac ctgaagaaag caaaaggcct gttctgagtg   5820
gggagacgcc agaggagcct cacggtcacg tccaacaaca ccactgcacc agggaaatgg   5880
atatatattt ttggactggt gtttttcaca aagtatttt caatcagagt tttcagaacc   5940
tgacattgtt aaagatactg cttgtcccgg agttgtgtat tttgtaaatg ttcaagggaa   6000
ctgtttggaa acttctttcc accattcagg aggttatcag aattaataaa agtatctgtt   6060
atgtgcactt aagccgcagc tgctatagat agcactgcct tcttgttcca gctaggcaat   6120
gcctttttt ttttttttga agcagttctc tttataaagt gttattttga tagtttgtgg   6180
```

```
attctaaaat atatatatat ttatataaac accatataag tcaaatatgt atttaacaaa   6240
gcaatatgta ttcattcact ttcaagattt gttttggtgt caaataaca tgaaaaggta    6300
gatggagttg cttctgttga attagctctg ccaccaatat gtatcttcat acacgtttgg   6360
aaatgtttcc tgcagcatta ggtatgactt gttctgagta ctgcttccgg tgctaaaatg   6420
aacaaagaat ttgtacttaa tggcatggac tctggagaat ctatgcgaat caacctttct   6480
accttaatat ctccccaaaa atgtatagtg ccttgttttt atgtacagtt tatatacaga   6540
aaagtttgct ctgcattttt gatgatggtt tggaacatta tctacaattt tactctcaaa   6600
tagtcaaaat aaaaacatct caatttctaa taccggttgt aaacaaacag tacacatgtc   6660
attttgtgat ataggactcc caaataaaag tatcagaata aacacaacaa ttaactggt    6719
```

<210> 40
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 40
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Met Val Val Glu His Pro Glu Phe Leu Lys Ala Gly Lys Glu Pro Gly
 1               5                  10                  15
Leu Gln Ile Trp Arg Val Glu Lys Phe Asp Leu Val Pro Val Pro Pro
                20                  25                  30
Asn Leu Tyr Gly Asp Phe Phe Thr Gly Asp Ala Tyr Val Ile Leu Lys
            35                  40                  45
Thr Val Gln Leu Arg Asn Gly Asn Leu Gln Tyr Asp Leu His Tyr Trp
        50                  55                  60
Leu Gly Asn Glu Cys Ser Gln Asp Glu Ser Gly Ala Ala Ala Ile Phe
65                  70                  75                  80
Thr Val Gln Leu Asp Asp Tyr Leu Asn Gly Arg Ala Val Gln His Arg
                85                  90                  95
Glu Val Gln Gly Phe Glu Ser Ser Thr Phe Ser Gly Tyr Phe Lys Ser
               100                 105                 110
Gly Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe Lys His Val
           115                 120                 125
Val Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val Lys Gly Arg
       130                 135                 140
Arg Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Asp Ser Phe Asn
145                 150                 155                 160
Asn Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile Tyr Gln Trp
               165                 170                 175
Cys Gly Ser Gly Ser Asn Lys Phe Glu Arg Leu Lys Ala Thr Gln Val
           180                 185                 190
Ser Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala Gln Val His
           195                 200                 205
Val Ser Glu Glu Glu Thr Glu Pro Glu Ala Met Leu Gln Val Leu Gly
       210                 215                 220
Pro Lys Pro Ala Leu Pro Glu Gly Thr Glu Asp Thr Ala Lys Glu Asp
225                 230                 235                 240
Ala Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser Asn Gly Ala
               245                 250                 255
Gly Ser Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro Phe Ala Gln
           260                 265                 270
Gly Pro Leu Arg Ser Glu Asp Cys Phe Ile Leu Asp His Gly Arg Asp
           275                 280                 285
Gly Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Met Glu Glu Arg
           290                 295                 300
```

```
Lys Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Ser Lys Met Gln Tyr
305                 310                 315                 320
Pro Arg Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly Glu Thr Pro
                325                 330                 335
Leu Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp Gln Thr Asp
                340·                345                 350
Gly Pro Gly Leu Gly Tyr Leu Ser Ser His Ile Ala Asn Val Glu Arg
            355                 360                 365
Val Pro Phe Asp Ala Gly Thr Leu His Thr Ser Thr Ala Met Ala Ala
    370                 375                 380
Gln His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln Ile Trp Arg
385                 390                 395                 400
Ile Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr Tyr Gly Gln
                405                 410                 415
Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr Arg His Gly
            420                 425                 430
Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala Gln Ser Thr
            435                 440                 445
Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln Leu Asp Glu
    450                 455                 460
Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln Gly Lys Glu
465                 470                 475                 480
Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met Ile Ile Tyr
                485                 490                 495
Lys Gly Gly Thr Ser Arg Asp Gly Gly Gln Thr Ala Pro Ala Ser Ile
                500                 505                 510
Arg Leu Phe Gln Val Arg Ala Ser Ser Ser Gly Ala Thr Arg Ala Val
                515                 520                 525
Glu Val Met Pro Lys Ser Gly Ala Leu Asn Ser Asn Asp Ala Phe Val
    530                 535                 540
Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Ala Gly Ala Ser
545                 550                 555                 560
Glu Ala Glu Lys Thr Ala Ala Gln Glu Leu Leu Lys Val Leu Arg Ser
                565                 570                 575
Gln His Val Gln Val Glu Glu Gly Ser Glu Pro Asp Gly Phe Trp Glu
                580                 585                 590
Ala Leu Gly Gly Lys Thr Ser Tyr Arg Thr Ser Pro Arg Leu Lys Asp
            595                 600                 605
Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys Ser Asn Arg
    610                 615                 620
Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu Met Gln Glu
625                 630                 635                 640
Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp Asp Gln Val
                645                 650                 655
Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys Thr Glu Ala
                660                 665                 670
Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala Asn Arg Asp
                675                 680                 685
Arg Arg Thr Pro Ile Thr Val Val Arg Gln Gly Phe Glu Pro Pro Ser
    690                 695                 700
Phe Val Gly Trp Phe Leu Gly Trp Asp Asn Asn Tyr Trp Ser Val Asp
705                 710                 715                 720
Pro Leu Asp Arg Ala Leu Ala Glu Leu Ala Ala
                725                 730
```

<210> 41
<211> 2447
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 41
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cctggcctgc agatctggcg tgtggagaag tttgacctgg tgcctgtgcc ccccaacctc    120
tatggagact tcttcacggg tgatgcctat gtcatcctga agactgtgca gctgaggaat    180
gggaatctgc agtatgacct ccactattgg ctgggcaatg aatgcagcca ggatgagagc    240
ggggctgctg ccatctttac tgtgcaactg gatgactacc tgaacggccg ggctgtgcag    300
caccgtgagg ttcagggctt tgagtcgtcc accttctccg gctacttcaa gtctggactt    360
aagtacaaga aaggaggtgt ggcatctgga ttcaaacacg tggtacccaa tgaggtggtg    420
gtccagaggc tcttccaggt caaaggacgc cgtgtagtcc gtgctactga ggtacctgtg    480
tcctgggaca gtttcaacaa tggcgactgc ttcattctgg acctgggaaa caatatctat    540
cagtggtgtg gctctggcag caacaaattt gaaaggctga aggccacaca ggtgtccaag    600
ggcatccggg acaacgagag gagtggccgt gctcaagtac acgtgtctga agaggagact    660
gagcccgagg cgatgctgca ggtgctgggc cccaagccgg ctctgcctga aggtaccgag    720
gacacagcca aggaagatgc agccaaccgc aagctggcca agctctacaa ggtctccaac    780
ggtgcaggta gcatgtcagt ctccctagtg gctgatgaga accccttcgc ccaggggccc    840
ctgagatctg aggactgctt catcctggac catggcagag atgggaaaat ctttgtttgg    900
aaaggcaagc aggccaacat ggaggagcgg aaggctgccc tcaaaacagc ctctgacttc    960
atctccaaga tgcagtaccc caggcagacc caggtttcag ttctcccaga gggcggtgag   1020
accccctctct ttaagcagtt cttcaagaac tggcgggacc cagaccagac agatggcccc   1080
ggcctgggct acctctccag ccacattgcc aacgtggagc gcgtaccttt cgatgccggc   1140
acgctgcaca cctccaccgc catggccgct cagcacggca tggatgatga tggaactggc   1200
cagaaacaga tctggagaat tgaaggttcc aacaaggtgc cagtggaccc tgccacatac   1260
ggacagttct atggaggcga cagctacatc attctgtaca actaccgcca cggtggccgc   1320
cagggacaga tcatctacaa ctggcagggt gctcagtcta cccaggatga ggttgctgct   1380
tctgccatcc tgactgccca gctggatgag gagctgggag gaactcctgt ccagagccga   1440
gtggtccaag gcaaagagcc tgcacacctc atgagcttgt ttggcgggaa gcccatgatc   1500
atctacaagg tggcacctc ccgtgatggt gggcagacag ctcctgccag tatccgcctc   1560
ttccaagtgc gtgccagcag ctctggagcc accagggctg tggaggtgat gcctaagtct   1620
ggtgctctga actccaacga tgcctttgtg ctgaaaaccc cctccgctgc ctacctgtgg   1680
gtgggcgcag gagccagtga ggcagagaag acggcggccc aggagcttct gaaggtcctt   1740
cggtcccagc atgtgcaggt ggaagaaggc agtgagccac atggcttctg ggaggctctg   1800
ggcgggaaga cgtcctaccg cacatccccc aggcttaagg acaagaagat ggatgcccat   1860
cctcctcgac tctttgcctg ctccaacagg atcggacgct ttgtgatcga agaggttcct   1920
ggcgagctta tgcaggaaga cctggctact gatgacgtca tgctcctgga cacctgggac   1980
caggtctttg tctgggttgg aaaaagactcc caggaagaag aaaagacgga agccttgact   2040
tctgctaagc ggtacatcga gacagatcca gcaaatcggg acaggcggac ccccatcaca   2100
gtcgttaggc agggctttga gcctccttcc ttcgtgggct ggttcctcgg ctgggacaac   2160
aactactggt cggtggatcc tttggaccgg gccttggctg agctggctgc ctgagtaagg   2220
accaagccat caatgtcacc aatcagtgcc tttgagggtt gtccatctcc caaagacatc   2280
atatggcaag caggaaaact atgatgtgtg cgcgcgtgtt tttgtttttg ttttttacgg   2340
tagccaaaac aagcccttgt ggaaactcag ggtctttaca gaattgcttc aaatgtctgt   2400
actttggaaa tgaaagccaa taaaagcttt ttgaagtgaa aaaaaaa               2447
```

<210> 42
<211> 928
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
     synthetic construct

<400> 42
```
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala Thr Ala Ala Ala Ala
1               5                   10                  15
Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro Glu Glu Asp
            20                  25                  30
```

```
Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu Val Arg Leu Glu
        35              40              45
Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu Cys Gln Lys Leu
        50              55              60
Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu Thr Trp Glu Lys
65              70              75              80
Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile Gln Lys Lys Lys
            85              90              95
Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala Val Asp Leu Asp Glu
        100             105             110
Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn Ile Glu Ile Ser Val
        115             120             125
His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr Ser Thr Lys Val
    130             135             140
Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp Val Leu Phe Ala
145             150             155             160
Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile Tyr Leu Thr Gln
            165             170             175
Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala Leu Val Leu Lys
        180             185             190
Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu Val Leu Gln Met
        195             200             205
Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu Cys Val Leu Asp
    210             215             220
Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys Glu Pro Tyr Lys
225             230             235             240
Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr Pro Arg Arg Gly
            245             250             255
Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu Asn Asp Thr Arg
        260             265             270
Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn Ile Asp Glu Val
    275             280             285
Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met Asn Ser Leu Gly
    290             295             300
Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn Leu Ser Lys Arg
305             310             315             320
Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp Ala Arg Leu Phe
            325             330             335
Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile Asp Ser Phe Glu
        340             345             350
Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu Glu Val Asn Val
        355             360             365
Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn Thr Ile Gln Gln
370             375             380
Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln Pro Ser Glu Asn Leu
385             390             395             400
Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro Lys Glu Ser Ile Leu
            405             410             415
Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys Glu Lys Phe Ala Lys
        420             425             430
Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser Gln Arg Tyr Lys Leu
        435             440             445
Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser Met Leu Lys Ser Glu
    450             455             460
Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys Leu Leu Asn Asp Asn
465             470             475             480
Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu Glu Val Val Met Ala
            485             490             495
Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp Ser Gly Thr Asp Leu
            500             505             510
```

```
Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu Lys Ala Phe Asp Phe
        515             520             525
Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu Gly Asn Leu Thr Arg
    530             535             540
Glu Met Ile Lys His Leu Glu Arg Cys Glu His Arg Ile Met Glu Ser
545             550             555             560
Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp Leu Ile Lys Gln Ser
            565             570             575
Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu Ser Ala Cys Pro Leu
            580             585             590
Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala Asp Met Tyr Leu Ser
            595             600             605
Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr Thr Arg Val Asn Ser
    610             615             620
Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala Phe Gln Thr Gln Lys
625             630             635             640
Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr Lys Lys Val Tyr Arg
            645             650             655
Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu Arg Leu Leu Ser Glu
            660             665             670
His Pro Glu Leu Glu His Ile Ile Trp Thr Leu Phe Gln His Thr Leu
            675             680             685
Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His Leu Asp Gln Ile Met
    690             695             700
Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys Asn Ile Asp Leu Lys
705             710             715             720
Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu Pro His Ala Val Gln
            725             730             735
Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu Glu Tyr Asp Ser Ile
            740             745             750
Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg Leu Lys Thr Asn Ile
            755             760             765
Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu Ser Pro Ile Pro His
    770             775             780
Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser Pro Leu Arg Ile Pro
785             790             795             800
Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser Pro Tyr Lys Ile Ser
            805             810             815
Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro Arg Ser Arg Ile Leu
            820             825             830
Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu Lys Phe Gln Lys Ile
    835             840             845
Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu Lys Arg Ser Ala Glu
    850             855             860
Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu Arg Phe Asp Ile Glu
865             870             875             880
Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu Pro Gly Glu Ser Lys
            885             890             895
Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr Arg Thr Arg Met Gln
            900             905             910
Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser Asn Lys Glu Glu Lys
            915             920             925
```

```
<210> 43
<211> 2994
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct
```

<400> 43

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ttccggtttt tctcagggga cgttgaaatt attttttgtaa cgggagtcgg gagaggacgg      60
ggcgtgcccc gcgtgcgcgc gcgtcgtcct ccccggcgct cctccacagc tcgctggctc     120
ccgccgcgga aaggcgtcat gccgcccaaa accccccgaa aaacggccgc caccgccgcc     180
gctgccgccg cggaacccccc ggcaccgccg ccgccgcccc ctcctgagga ggacccagag     240
caggacagcg gcccggagga cctgcctctc gtcaggcttg agtttgaaga aacagaagaa     300
cctgatttta ctgcattatg tcagaaatta aagataccag atcatgtcag agagagagct     360
tggttaactt gggagaaagt ttcatctgtg gatggagtat tgggaggtta tattcaaaag     420
aaaaaggaac tgtggggaat ctgtatcttt attgcagcag ttgacctaga tgagatgtcg     480
ttcactttta ctgagctaca gaaaaacata gaaatcagtg tccataaatt ctttaactta     540
ctaaaagaaa ttgataccag taccaaagtt gataatgcta tgtcaagact gttgaagaag     600
tatgatgtat tgtttgcact cttcagcaaa ttggaaagga catgtgaact tatatatttg     660
acacaaccca gcagttcgat atctactgaa ataaattctg cattggtgct aaaagtttct     720
tggatcacat ttttattagc taaaggggaa gtattacaaa tggaagatga tctggtgatt     780
tcatttcagt taatgctatg tgtccttgac tatttttatta aactctcacc tcccatgttg     840
ctcaaagaac catataaaac agctgttata cccattaatg gttcacctcg aacacccagg     900
cgaggtcaga acaggagtgc acggatagca aaacaactag aaaatgatac aagaattatt     960
gaagttctct gtaaagaaca tgaatgtaat atagatgagg tgaaaaatgt ttatttcaaa    1020
aattttatac cttttatgaa ttctcttgga cttgtaacat ctaatggact tccagaggtt    1080
gaaaatcttt ctaaacgata cgaagaaatt tatcttaaaa ataaagatct agatgcaaga    1140
ttattttttgg atcatgataa aactcttcag actgattcta tagacagttt tgaaacacag    1200
agaacaccac gaaaaagtaa ccttgatgaa gaggtgaatg taattcctcc acacactcca    1260
gttaggactg ttatgaacac tatccaacaa ttaatgatga ttttaaattc agcaagtgat    1320
caaccttcag aaaatctgat ttcctatttt aacaactgca cagtgaatcc aaaagaaagt    1380
atactgaaaa gagtgaagga tataggatac atctttaaag agaaatttgc taaagctgtg    1440
ggacagggtt gtgtcgaaat tggatcacag cgatacaaac ttggagttcg cttgtattac    1500
cgagtaatgg aatccatgct taaatcagaa gaagaacgat tatccattca aaattttagc    1560
aaacttctga atgacaacat ttttcatatg tctttattgg cgtgcgctct tgaggttgta    1620
atggccacat atagcagaag tacatctcag aatcttgatt ctggaacaga tttgtctttc    1680
ccatggattc tgaatgtgct taatttaaaa gcctttgatt tttacaaagt gatcgaaagt    1740
tttatcaaag cagaaggcaa cttgacaaga gaaatgataa aacatttaga acgatgtgaa    1800
catcgaatca tggaatccct tgcatggctc tcagattcac ctttatttga tcttattaaa    1860
caatcaaagg accgagaagg accaactgat caccttgaat ctgcttgtcc tcttaatctt    1920
cctctccaga ataatcacac tgcagcagat atgtatcttt ctcctgtaag atctccaaag    1980
aaaaaaggtt caactacgcg tgtaaattct actgcaaatg cagagacaca agcaacctca    2040
gccttccaga cccagaagcc attgaaatct acctctcttt cactgtttta taaaaaagtg    2100
tatcggctag cctatctccg gctaaataca ctttgtgaac gccttctgtc tgagcaccca    2160
gaattagaac atatcatctg gacccttttc cagcacaccc tgcagaatga gtatgaactc    2220
atgagagaca ggcatttgga ccaaattatg atgtgttcca tgtatggcat atgcaaagtg    2280
aagaatatag accttaaatt caaaatcatt gtaacagcat acaaggatct tcctcatgct    2340
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ttctataact cggtcttcat gcagagactg aaaacaaata ttttgcagta tgcttccacc    2460
aggccccccta ccttgtcacc aatacctcac attcctcgaa gcccttacaa gtttcctagt    2520
tcacccttac ggattcctgg agggaacatc tatatttcac ccctgaagag tccatataaa    2580
atttcagaag gtctgccaac accaacaaaa atgactccaa gatcaagaat cttagtatca    2640
attggtgaat cattcgggac ttctgagaag ttccagaaaa taaatcagat ggtatgtaac    2700
agcgaccgtg tgctcaaaag aagtgctgaa ggaagcaacc ctcctaaacc actgaaaaaa    2760
ctacgctttg atattgaagg atcagatgaa gcagatggaa gtaaacatct cccaggagag    2820
tccaaatttc agcagaaact ggcagaaatg acttctactc gaacacgaat gcaaaagcag    2880
aaaatgaatg atagcatgga tacctcaaac aaggaagaga atgaggatc tcaggacctt    2940
ggtggacact gtgtacacct ctggattcat tgtctctcac agatgtgact gtat         2994
```

<210> 44
<211> 782
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 44

Met	Ala	Pro	His	Arg	Pro	Ala	Pro	Ala	Leu	Leu	Cys	Ala	Leu	Ser	Leu
1				5					10					15	
Ala	Leu	Cys	Ala	Leu	Ser	Leu	Pro	Val	Arg	Ala	Ala	Thr	Ala	Ser	Arg
			20					25					30		
Gly	Ala	Ser	Gln	Ala	Gly	Ala	Pro	Gln	Gly	Arg	Val	Pro	Glu	Ala	Arg
			35				40					45			
Pro	Asn	Ser	Met	Val	Val	Glu	His	Pro	Glu	Phe	Leu	Lys	Ala	Gly	Lys
	50				55					60					
Glu	Pro	Gly	Leu	Gln	Ile	Trp	Arg	Val	Glu	Lys	Phe	Asp	Leu	Val	Pro
65					70				75						80
Val	Pro	Thr	Asn	Leu	Tyr	Gly	Asp	Phe	Phe	Thr	Gly	Asp	Ala	Tyr	Val
				85					90					95	
Ile	Leu	Lys	Thr	Val	Gln	Leu	Arg	Asn	Gly	Asn	Leu	Gln	Tyr	Asp	Leu
			100					105					110		
His	Tyr	Trp	Leu	Gly	Asn	Glu	Cys	Ser	Gln	Asp	Glu	Ser	Gly	Ala	Ala
		115					120					125			
Ala	Ile	Phe	Thr	Val	Gln	Leu	Asp	Asp	Tyr	Leu	Asn	Gly	Arg	Ala	Val
	130					135					140				
Gln	His	Arg	Glu	Val	Gln	Gly	Phe	Glu	Ser	Ala	Thr	Phe	Leu	Gly	Tyr
145					150					155					160
Phe	Lys	Ser	Gly	Leu	Lys	Tyr	Lys	Lys	Gly	Gly	Val	Ala	Ser	Gly	Phe
				165					170					175	
Lys	His	Val	Val	Pro	Asn	Glu	Val	Val	Val	Gln	Arg	Leu	Phe	Gln	Val
			180					185					190		
Lys	Gly	Arg	Arg	Val	Val	Arg	Ala	Thr	Glu	Val	Pro	Val	Ser	Trp	Glu
			195					200					205		
Ser	Phe	Asn	Asn	Gly	Asp	Cys	Phe	Ile	Leu	Asp	Leu	Gly	Asn	Asn	Ile
	210					215					220				
His	Gln	Trp	Cys	Gly	Ser	Asn	Ser	Asn	Arg	Tyr	Glu	Arg	Leu	Lys	Ala
225					230					235					240
Thr	Gln	Val	Ser	Lys	Gly	Ile	Arg	Asp	Asn	Glu	Arg	Ser	Gly	Arg	Ala
				245					250					255	
Arg	Val	His	Val	Ser	Glu	Glu	Gly	Thr	Glu	Pro	Glu	Ala	Met	Leu	Gln
			260					265					270		
Val	Leu	Gly	Pro	Lys	Pro	Ala	Leu	Pro	Ala	Gly	Thr	Glu	Asp	Thr	Ala
		275					280					285			
Lys	Glu	Asp	Ala	Ala	Asn	Arg	Lys	Leu	Ala	Lys	Leu	Tyr	Lys	Val	Ser
	290					295					300				
Asn	Gly	Ala	Gly	Thr	Met	Ser	Val	Ser	Leu	Val	Ala	Asp	Glu	Asn	Pro
305					310					315					320
Phe	Ala	Gln	Gly	Ala	Leu	Lys	Ser	Glu	Asp	Cys	Phe	Ile	Leu	Asp	His
			325					330					335		
Gly	Lys	Asp	Gly	Lys	Ile	Phe	Val	Trp	Lys	Gly	Lys	Gln	Ala	Asn	Thr
			340					345					350		
Glu	Glu	Arg	Lys	Ala	Ala	Leu	Lys	Thr	Ala	Ser	Asp	Phe	Ile	Thr	Lys
		355					360					365			
Met	Asp	Tyr	Pro	Lys	Gln	Thr	Gln	Val	Ser	Val	Leu	Pro	Glu	Gly	Gly
	370					375					380				
Glu	Thr	Pro	Leu	Phe	Lys	Gln	Phe	Phe	Lys	Asn	Trp	Arg	Asp	Pro	Asp
385					390					395					400
Gln	Thr	Asp	Gly	Leu	Gly	Leu	Ser	Tyr	Leu	Ser	Ser	His	Ile	Ala	Asn
			405					410					415		
Val	Glu	Arg	Val	Pro	Phe	Asp	Ala	Ala	Thr	Leu	His	Thr	Ser	Thr	Ala
			420					425					430		
Met	Ala	Ala	Gln	His	Gly	Met	Asp	Asp	Asp	Gly	Thr	Gly	Gln	Lys	Gln
		435					440					445			
Ile	Trp	Arg	Ile	Glu	Gly	Ser	Asn	Lys	Val	Pro	Val	Asp	Pro	Ala	Thr
	450					455					460				

```
Tyr Gly Gln Phe Tyr Gly Gly Asp Ser Tyr Ile Ile Leu Tyr Asn Tyr
465                 470                 475                 480
Arg His Gly Gly Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala
            485                 490                 495
Gln Ser Thr Gln Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln
            500                 505                 510
Leu Asp Glu Glu Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln
        515                 520                 525
Gly Lys Glu Pro Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met
        530                 535                 540
Ile Ile Tyr Lys Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro
545                 550                 555                 560
Ala Ser Thr Arg Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr
            565                 570                 575
Arg Ala Val Glu Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp
            580                 585                 590
Ala Phe Val Leu Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr
            595                 600                 605
Gly Ala Ser Glu Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val
        610                 615                 620
Leu Arg Ala Gln Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly
625                 630                 635                 640
Phe Trp Glu Ala Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg
            645                 650                 655
Leu Lys Asp Lys Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys
            660                 665                 670
Ser Asn Lys Ile Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu
            675                 680                 685
Met Gln Glu Asp Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp
    690                 695                 700
Asp Gln Val Phe Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys
705                 710                 715                 720
Thr Glu Ala Leu Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala
            725                 730                 735
Asn Arg Asp Arg Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu
            740                 745                 750
Pro Pro Ser Phe Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp
            755                 760                 765
Ser Val Asp Pro Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
            770                 775                 780
```

```
<210> 45
<211> 2663
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 45
ccaccatggc tccgcaccgc cccgcgcccg cgctgctttg cgcgctgtcc ctggcgctgt        60
gcgcgctgtc gctgcccgtc cgcgcggcca ctgcgtcgcg ggggcgtcc caggcggggg       120
cgccccaggg gcgggtgccc gaggcgcggc ccaacagcat ggtggtggaa caccccgagt       180
tcctcaaggc agggaaggag cctggcctgc agatctggcg tgtggagaag ttcgatctgg       240
tgcccgtgcc caccaacctt tatggagact tcttcacggg cgacgcctac gtcatcctga       300
agacagtgca gctgaggaac ggaaatctgc agtatgacct ccactactgg ctgggcaatg       360
agtgcagcca ggatgagagc ggggcggccg ccatctttac cgtgcagctg gatgactacc       420
tgaacggccg ggccgtgcag caccgtgagg tccagggctt cgagtcggcc accttcctag       480
gctacttcaa gtctggcctg aagtacaaga aaggaggtgt ggcatcagga ttcaagcacg       540
tggtacccaa cgaggtggtg gtgcagagac tcttccaggt caaagggcgg cgtgtggtcc       600
```

79

```
gtgccaccga ggtacctgtg tcctgggaga gcttcaacaa tggcgactgc ttcatcctgg       660
acctgggcaa caacatccac cagtggtgtg gttccaacag caatcggtat gaaagactga       720
aggccacaca ggtgtccaag ggcatccggg acaacgagcg gagtggccgg gcccgagtgc       780
acgtgtctga ggagggcact gagcccgagg cgatgctcca ggtgctgggc cccaagccgg       840
ctctgcctgc aggtaccgag gacaccgcca aggaggatgc ggccaaccgc aagctggcca       900
agctctacaa ggtctccaat ggtgcaggga ccatgtccgt ctccctcgtg gctgatgaga       960
accccttcgc ccagggggcc ctgaagtcag aggactgctt catcctggac cacggcaaag      1020
atgggaaaat ctttgtctgg aaaggcaagc aggcaaacac ggaggagagg aaggctgccc      1080
tcaaaacagc ctctgacttc atcaccaaga tggactaccc caagcagact caggtctcgg      1140
tccttcctga gggcggtgag accccactgt tcaagcagtt cttcaagaac tggcgggacc      1200
cagaccagac agatggcctg ggcttgtcct acctttccag ccatatcgcc aacgtggagc      1260
gggtgccctt cgacgccgcc accctgcaca cctccactgc catggccgcc agcacggca       1320
tggatgacga tggcacaggc cagaaacaga tctggagaat cgaaggttcc aacaaggtgc      1380
ccgtggaccc tgccacatat ggacagttct atggaggcga cagctacatc attctgtaca      1440
actaccgcca tggtggccgc caggggcaga taatctataa ctggcagggt gcccagtcta      1500
cccaggatga ggtcgctgca tctgccatcc tgactgctca gctggatgag gagctgggag      1560
gtaccccctgt ccagagccgt gtggtccaag gcaaggagcc cgcccacctc atgagcctgt      1620
ttggtgggaa gcccatgatc atctacaagg gcggcacctc ccgcgagggc gggcagacag      1680
cccctgccag cacccgcctc ttccaggtcc gcgccaacag cgctggagcc acccgggctg      1740
ttgaggtatt gcctaaggct ggtgcactga actccaacga tgcctttgtt ctgaaaaccc      1800
cctcagccgc ctacctgtgg gtgggtacag gagccagcga ggcagagaag acggggggcc      1860
aggagctgct cagggtgctg cgggcccaac ctgtgcaggt ggcagaaggc agcgagccag      1920
atggcttctg ggaggccctg ggcgggaagg ctgcctaccg cacatcccca cggctgaagg      1980
acaagaagat ggatgcccat cctcctcgcc tctttgcctg ctccaacaag attggacgtt      2040
ttgtgatcga agaggttcct ggtgagctca tgcaggaaga cctggcaacg gatgacgtca      2100
tgcttctgga cacctgggac caggtctttg tctgggttgg aaaggattct caagaagaag      2160
aaaagacaga agccttgact tctgctaagc ggtacatcga gacggaccca gccaatcggg      2220
atcggcggac gcccatcacc gtggtgaagc aaggctttga gcctccctcc tttgtgggct      2280
ggttccttgg ctgggatgat gattactggt ctgtggaccc cttggacagg gccatggctg      2340
agctggctgc ctgaggaggg gcagggccca cccatgtcac cggtcagtgc cttttggaac      2400
tgtccttccc tcaaagaggc cttagagcga gcagagcagc tctgctatga gtgtgtgtgt      2460
gtgtgtgtgt tgtttctttt tttttttttt acagtatcca aaaatagccc tgcaaaaatt      2520
cagagtcctt gcaaaattgt ctaaaatgtc agtgtttggg aaattaaatc caataaaaac      2580
attttgaagt gtgaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa      2640
aaaaaaaaaa aaaaaaaaaa aaa                                             2663
```

```
<210> 46
<211> 1441
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 46
Met Ser Gly Leu Gly Asp Ser Ser Ser Asp Pro Ala Asn Pro Asp Ser
1               5                   10                  15
His Lys Arg Lys Gly Ser Pro Cys Asp Thr Leu Ala Ser Ser Thr Glu
            20                  25                  30
Lys Arg Arg Arg Glu Gln Glu Asn Lys Tyr Leu Glu Glu Leu Ala Glu
        35                  40                  45
Leu Leu Ser Ala Asn Ile Ser Asp Ile Asp Ser Leu Ser Val Lys Pro
    50                  55                  60
Asp Lys Cys Lys Ile Leu Lys Lys Thr Val Asp Gln Ile Gln Leu Met
65                  70                  75                  80
Lys Arg Met Glu Gln Glu Lys Ser Thr Thr Asp Asp Asp Val Gln Lys
                85                  90                  95
Ser Asp Ile Ser Ser Ser Ser Gln Gly Val Ile Glu Lys Glu Ser Leu
            100                 105                 110
```

```
Gly Pro Leu Leu Leu Glu Ala Leu Asp Gly Phe Phe Phe Val Val Asn
        115                 120                 125
Cys Glu Gly Arg Ile Val Phe Val Ser Glu Asn Val Thr Ser Tyr Leu
    130             135                 140
Gly Tyr Asn Gln Glu Glu Leu Met Asn Thr Ser Val Tyr Ser Ile Leu
145             150                 155                 160
His Val Gly Asp His Ala Glu Phe Val Lys Asn Leu Leu Pro Lys Ser
                165                 170                 175
Leu Val Asn Gly Val Pro Trp Pro Gln Glu Ala Thr Arg Arg Asn Ser
            180             185                 190
His Thr Phe Asn Cys Arg Met Leu Ile His Pro Pro Asp Glu Pro Gly
        195                 200                 205
Thr Glu Asn Gln Glu Ala Cys Gln Arg Tyr Glu Val Met Gln Cys Phe
    210             215                 220
Thr Val Ser Gln Pro Lys Ser Ile Gln Glu Asp Gly Glu Asp Phe Gln
225             230                 235                 240
Ser Cys Leu Ile Cys Ile Ala Arg Arg Leu Pro Arg Pro Pro Ala Ile
            245                 250                 255
Thr Gly Val Glu Ser Phe Met Thr Lys Gln Asp Thr Thr Gly Lys Ile
            260                 265                 270
Ile Ser Ile Asp Thr Ser Ser Leu Arg Ala Ala Gly Arg Thr Gly Trp
    275                 280                 285
Glu Asp Leu Val Arg Lys Cys Ile Tyr Ala Phe Phe Gln Pro Gln Gly
    290             295                 300
Arg Glu Pro Ser Tyr Ala Arg Gln Leu Phe Gln Glu Val Met Thr Arg
305             310                 315                 320
Gly Thr Ala Ser Ser Pro Ser Tyr Arg Phe Ile Leu Asn Asp Gly Thr
            325                 330                 335
Met Leu Ser Ala His Thr Lys Cys Lys Leu Cys Tyr Pro Gln Ser Pro
            340                 345                 350
Asp Met Gln Pro Phe Ile Met Gly Ile His Ile Ile Asp Arg Glu His
        355                 360                 365
Ser Gly Leu Ser Pro Gln Asp Asp Thr Asn Ser Gly Met Ser Ile Pro
    370                 375                 380
Arg Val Asn Pro Ser Val Asn Pro Ser Ile Ser Pro Ala His Gly Val
385             390                 395                 400
Ala Arg Ser Ser Thr Leu Pro Pro Ser Asn Ser Asn Met Val Ser Thr
            405                 410                 415
Arg Ile Asn Arg Gln Gln Ser Ser Asp Leu His Ser Ser Ser His Ser
            420                 425                 430
Asn Ser Ser Asn Ser Gln Gly Ser Phe Gly Cys Ser Pro Gly Ser Gln
    435                 440                 445
Ile Val Ala Asn Val Ala Leu Asn Lys Gly Gln Ala Ser Ser Gln Ser
    450                 455                 460
Ser Lys Pro Ser Leu Asn Leu Asn Asn Pro Pro Met Glu Gly Thr Gly
465                 470                 475                 480
Ile Ser Leu Ala Gln Phe Met Ser Pro Arg Arg Gln Val Thr Ser Gly
            485                 490                 495
Leu Ala Thr Arg Pro Arg Met Pro Asn Asn Ser Phe Pro Pro Asn Ile
            500                 505                 510
Ser Thr Leu Ser Ser Pro Val Gly Met Thr Ser Ser Ala Cys Asn Asn
    515                 520                 525
Asn Asn Arg Ser Tyr Ser Asn Ile Pro Val Thr Ser Leu Gln Gly Met
    530                 535                 540
Asn Glu Gly Pro Asn Asn Ser Val Gly Phe Ser Ala Ser Ser Pro Val
545                 550                 555                 560
Leu Arg Gln Met Ser Ser Gln Asn Ser Pro Ser Arg Leu Asn Ile Gln
            565                 570                 575
Pro Ala Lys Ala Glu Ser Lys Asp Asn Lys Glu Ile Ala Ser Thr Leu
            580                 585                 590
```

```
Asn Glu Met Ile Gln Ser Asp Asn Ser Ser Ser Asp Gly Lys Pro Leu
        595                 600                 605
Asp Ser Gly Leu Leu His Asn Asn Asp Arg Leu Ser Asp Gly Asp Ser
        610                 615                 620
Lys Tyr Ser Gln Thr Ser His Lys Leu Val Gln Leu Leu Thr Thr Thr
625                 630                 635                 640
Ala Glu Gln Gln Leu Arg His Ala Asp Ile Asp Thr Ser Cys Lys Asp
                645                 650                 655
Val Leu Ser Cys Thr Gly Thr Ser Asn Ser Ala Ser Ala Asn Ser Ser
                660                 665                 670
Gly Gly Ser Cys Pro Ser Ser His Ser Ser Leu Thr Ala Arg His Lys
            675                 680                 685
Ile Leu His Arg Leu Leu Gln Glu Gly Ser Pro Ser Asp Ile Thr Thr
        690                 695                 700
Leu Ser Val Glu Pro Asp Lys Lys Asp Ser Ala Ser Thr Ser Val Ser
705                 710                 715                 720
Val Thr Gly Gln Val Gln Gly Asn Ser Ser Ile Lys Leu Glu Leu Asp
                725                 730                 735
Ala Ser Lys Lys Lys Glu Ser Lys Asp His Gln Leu Leu Arg Tyr Leu
                740                 745                 750
Leu Asp Lys Asp Glu Lys Asp Leu Arg Ser Thr Pro Asn Leu Ser Leu
            755                 760                 765
Asp Asp Val Lys Val Lys Val Glu Lys Lys Glu Gln Met Asp Pro Cys
        770                 775                 780
Asn Thr Asn Pro Thr Pro Met Thr Lys Pro Thr Pro Glu Glu Ile Lys
785                 790                 795                 800
Leu Glu Ala Gln Ser Gln Phe Thr Ala Asp Leu Asp Gln Phe Asp Gln
                805                 810                 815
Leu Leu Pro Thr Leu Glu Lys Ala Ala Gln Leu Pro Gly Leu Cys Glu
            820                 825                 830
Thr Asp Arg Met Asp Gly Ala Val Thr Ser Val Thr Ile Lys Ser Glu
        835                 840                 845
Ile Leu Pro Ala Ser Leu Gln Ser Ala Thr Ala Arg Pro Thr Ser Arg
    850                 855                 860
Leu Asn Arg Leu Pro Glu Leu Glu Leu Glu Ala Ile Asp Asn Gln Phe
865                 870                 875                 880
Gly Gln Pro Gly Thr Gly Asp Gln Ile Pro Trp Thr Asn Asn Thr Val
            885                 890                 895
Thr Ala Ile Asn Gln Ser Lys Ser Glu Asp Gln Cys Ile Ser Ser Gln
        900                 905                 910
Leu Asp Glu Leu Leu Cys Pro Pro Thr Thr Val Glu Gly Arg Asn Asp
        915                 920                 925
Glu Lys Ala Leu Leu Glu Gln Leu Val Ser Phe Leu Ser Gly Lys Asp
    930                 935                 940
Glu Thr Glu Leu Ala Glu Leu Asp Arg Ala Leu Gly Ile Asp Lys Leu
945                 950                 955                 960
Val Gln Gly Gly Gly Leu Asp Val Leu Ser Glu Arg Phe Pro Pro Gln
                965                 970                 975
Gln Ala Thr Pro Pro Leu Ile Met Glu Glu Arg Pro Asn Leu Tyr Ser
            980                 985                 990
Gln Pro Tyr Ser Ser Pro Phe Pro Thr Ala Asn Leu Pro Ser Pro Phe
        995                 1000                1005
Gln Gly Met Val Arg Gln Lys Pro Ser Leu Gly Thr Met Pro Val Gln
    1010                1015                1020
Val Thr Pro Pro Arg Gly Ala Phe Ser Pro Gly Met Gly Met Gln Pro
1025                1030                1035                1040
Arg Gln Thr Leu Asn Arg Pro Pro Ala Ala Pro Asn Gln Leu Arg Leu
                1045                1050                1055
Gln Leu Gln Gln Arg Leu Gln Gly Gln Gln Leu Ile His Gln Asn
        1060                1065                1070
```

```
Arg Gln Ala Ile Leu Asn Gln Phe Ala Ala Thr Ala Pro Val Gly Ile
    1075                1080                1085
Asn Met Arg Ser Gly Met Gln Gln Gln Ile Thr Pro Gln Pro Pro Leu
    1090                1095                1100
Asn Ala Gln Met Leu Ala Gln Arg Gln Arg Glu Leu Tyr Ser Gln Gln
1105                1110                1115                1120
His Arg Gln Arg Gln Leu Ile Gln Gln Gln Arg Ala Met Leu Met Arg
                1125                1130                1135
Gln Gln Ser Phe Gly Asn Asn Leu Pro Pro Ser Ser Gly Leu Pro Val
                1140                1145                1150
Gln Thr Gly Asn Pro Arg Leu Pro Gln Gly Ala Pro Gln Gln Phe Pro
                1155                1160                1165
Tyr Pro Pro Asn Tyr Gly Thr Asn Pro Gly Thr Pro Pro Ala Ser Thr
    1170                1175                1180
Ser Pro Phe Ser Gln Leu Ala Ala Asn Pro Glu Ala Ser Leu Ala Asn
1185                1190                1195                1200
Arg Asn Ser Met Val Ser Arg Gly Met Thr Gly Asn Ile Gly Gly Gln
                1205                1210                1215
Phe Gly Thr Gly Ile Asn Pro Gln Met Gln Gln Asn Val Phe Gln Tyr
                1220                1225                1230
Pro Gly Ala Gly Met Val Pro Gln Gly Glu Ala Asn Phe Ala Pro Ser
    1235                1240                1245
Leu Ser Pro Gly Ser Ser Met Val Pro Met Pro Ile Pro Pro Pro Gln
    1250                1255                1260
Ser Ser Leu Leu Gln Gln Thr Pro Pro Ala Ser Gly Tyr Gln Ser Pro
1265                1270                1275                1280
Asp Met Lys Ala Trp Gln Gln Gly Ala Ile Gly Asn Asn Asn Val Phe
                1285                1290                1295
Ser Gln Ala Val Gln Asn Gln Pro Thr Pro Ala Gln Pro Gly Val Tyr
                1300                1305                1310
Asn Asn Met Ser Ile Thr Val Ser Met Ala Gly Gly Asn Thr Asn Val
                1315                1320                1325
Gln Asn Met Asn Pro Met Met Ala Gln Met Gln Met Ser Ser Leu Gln
    1330                1335                1340
Met Pro Gly Met Asn Thr Val Cys Pro Glu Gln Ile Asn Asp Pro Ala
1345                1350                1355                1360
Leu Arg His Thr Gly Leu Tyr Cys Asn Gln Leu Ser Ser Thr Asp Leu
                1365                1370                1375
Leu Lys Thr Glu Ala Asp Gly Thr Gln Gln Val Gln Gln Val Gln Val
                1380                1385                1390
Phe Ala Asp Val Gln Cys Thr Val Asn Leu Val Gly Gly Asp Pro Tyr
    1395                1400                1405
Leu Asn Gln Pro Gly Pro Leu Gly Thr Gln Lys Pro Thr Ser Gly Pro
    1410                1415                1420
Gln Thr Pro Gln Ala Gln Gln Lys Ser Leu Arg Gln Gln Leu Leu Thr
1425                1430                1435                1440
Glu
```

```
<210> 47
<211> 4547
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 47
cggatccact agtccagtgt ggtggaattc ggcttcatca tcatgagtgg ccttggggac        60
agttcatccg accctgctaa cccagactca cataagagga aaggatcgcc atgtgacaca       120
```

```
ctggcatcaa gcacggaaaa gaggcgcagg gagcaagaaa ataaatattt agaagaacta    180
gctgagttac tgtctgccaa cattagtgac attgacagct tgagtgtaaa accagacaaa    240
tgcaagattt tgaagaaaac agtcgatcag atacagctaa tgaagagaat ggaacaagag    300
aaatcaacaa ctgatgacga tgtacagaaa tcagacatct catcaagtag tcaaggagtg    360
atagaaaagg aatccttggg acctcttctt ttggaggctt tggatggatt tttctttgtt    420
gtgaactgtg aagggagaat tgtatttgtg tcagagaatg taaccagcta cttaggttac    480
aatcaggagg aattaatgaa tacgagcgtc tacagcatac tgcacgtggg ggatcatgca    540
gaatttgtga agaatctgct accaaaatca ctagtaaatg gagttccttg gcctcaagag    600
gcaacacgac gaaatagcca taccttaaac tgcaggatgc taattcaccc tccagatgag    660
ccagggaccg agaaccaaga agcttgccag cgttatgaag taatgcagtg tttcactgtg    720
tcacagccaa aatcaattca agaggatgga gaagatttcc agtcatgtct gatttgtatt    780
gcacggcgat tacctcggcc tccagctatt acgggtgtag aatcctttat gaccaagcaa    840
gatactacag gtaaaatcat ctctattgat actagttccc tgagagctgc tggcagaact    900
ggttgggaag atttagtgag gaagtgcatt tatgcttttt tccaacctca gggcagagaa    960
ccatcttatg ccagacagct gttccaagaa gtgatgactc gtggcactgc ctccagcccc   1020
tcctatagat tcatattgaa tgatgggaca atgcttagcg cccacaccaa gtgtaaactt   1080
tgctaccctc aaagtccaga catgcaacct ttcatcatgg gaattcatat catcgacagg   1140
gagcacagtg ggctttctcc tcaagatgac actaattctg gaatgtcaat tccccgagta   1200
aatccctcgg tcaatcctag tatctctcca gctcatggtg tggctcgttc atccacattg   1260
ccaccatcca acagcaacat ggtatccacc agaataaacc gccagcagag ctcagacctt   1320
catagcagca gtcatagtaa ttctagcaac agccaaggaa gtttcggatg ctcacccgga   1380
agtcagattg tagccaatgt tgccttaaac aaaggacagg ccagttcaca gagcagtaaa   1440
ccctctttaa acctcaataa tcctcctatg gaaggtacag gaatatccct agcacagttc   1500
atgtctccaa ggagacaggt tacttctgga ttggcaacaa ggcccaggat gccaaacaat   1560
tcctttcctc ctaatatttc gacattaagc tctcccgttg gcatgacaag tagtgcctgt   1620
aataataata accgatctta ttcaaacatc ccagtaacat ctttacaggg tatgaatgaa   1680
ggacccaata actccgttgg cttctctgcc agttctccag tcctcaggca gatgagctca   1740
cagaattcac ctagcagatt aaatatacaa ccagcaaaag ctgagtccaa agataacaaa   1800
gagattgcct caactttaaa tgaaatgatt caatctgaca acagctctag tgatggcaaa   1860
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84

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